



SEQUENCE LISTING

GENERAL INFORMATION:

RECEIVED
AUG 22 2002
TECH CENTER 1600/2900

J3
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Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
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(ii) TITLE OF INVENTION: Telomerase Reverse Transcriptase

(iii) NUMBER OF SEQUENCES: 479

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: San Francisco
(D) STATE: California
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(F) ZIP: 94111-3834

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/974,584
(B) FILING DATE: 19-NOV-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/724,643
(B) FILING DATE: 01-OCT-1996

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/844,419
(B) FILING DATE: 18-APR-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/846,017
(B) FILING DATE: 25-APR-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/851,843
(B) FILING DATE: 06-MAY-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/854,050
(B) FILING DATE: 09-MAY-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/911,312
(B) FILING DATE: 14-AUG-1997

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/912,951
(B) FILING DATE: 14-AUG-1997

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/915,503
(B) FILING DATE: 14-AUG-1997

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: WO PCT/US97/17618
(B) FILING DATE: 01-OCT-1997

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: WO PCT/US97/17885
(B) FILING DATE: 01-OCT-1997

(viii) ATTORNEY/AGENT INFORMATION:
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(C) REFERENCE/DOCKET NUMBER: 015389-002950US

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (415) 576-0200
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3279 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 101..3196
(D) OTHER INFORMATION: /codon= (seq: "tga", aa: Cys)
/note= "Euplotes aediculatus 123 kD
telomerase subunit"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAAACCCCAA AACCCAAAAA CCCCTTTAG AGCCCTGCAG TTGGAAATAT AACCTCAGTA	60
TTAATAAGCT CAGATTAAAT ATATTAATTA CAAAACCTAA ATG GAG GTT GAT GTT Met Glu Val Asp Val	115
1 5	
GAT AAT CAA GCT GAT AAT CAT GGC ATT CAC TCA GCT CTT AAG ACT TGT Asp Asn Gln Ala Asp Asn His Gly Ile His Ser Ala Leu Lys Thr Cys	163
10 15 20	
GAA GAA ATT AAA GAA GCT AAA ACG TTG TAC TCT TGG ATC CAG AAA GTT Glu Glu Ile Lys Glu Ala Lys Thr Leu Tyr Ser Trp Ile Gln Lys Val	211
25 30 35	

ATT AGA TGA AGA AAT CAA TCT CAA AGT CAT TAT AAA GAT TTA GAA GAT Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr Lys Asp Leu Glu Asp 40	45	50	259
ATT AAA ATA TTT GCG CAG ACA AAT ATT GTT GCT ACT CCA CGA GAC TAT Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala Thr Pro Arg Asp Tyr 55	60	65	307
AAT GAA GAA GAT TTT AAA GTT ATT GCA AGA AAA GAA GTA TTT TCA ACT Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys Glu Val Phe Ser Thr 70	75	80	355
GGA CTA ATG ATC GAA CTT ATT GAC AAA TGC TTA GTT GAA CTT CTT TCA Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu Val Glu Leu Leu Ser 90	95	100	403
TCA AGC GAT GTT TCA GAT AGA CAA AAA CTT CAA TGA TTT GGA TTT CAA Ser Ser Asp Val Ser Asp Arg Gln Lys Leu Gln Cys Phe Gly Phe Gln 105	110	115	451
CTT AAG GGA AAT CAA TTA GCA AAG ACC CAT TTA TTA ACA GCT CTT TCA Leu Lys Gly Asn Gln Leu Ala Lys Thr His Leu Leu Thr Ala Leu Ser 120	125	130	499
ACT CAA AAG CAG TAT TTC TTT CAA GAC GAA TGG AAC CAA GTT AGA GCA Thr Gln Lys Gln Tyr Phe Phe Gln Asp Glu Trp Asn Gln Val Arg Ala 135	140	145	547
ATG ATT GGA AAT GAG CTC TTC CGA CAT CTC TAC ACT AAA TAT TTA ATA Met Ile Gly Asn Glu Leu Phe Arg His Leu Tyr Thr Lys Tyr Leu Ile 150	155	160	595
TTC CAG CGA ACT TCT GAA GGA ACT CTT GTT CAA TTT TGC GGG AAT AAC Phe Gln Arg Thr Ser Glu Gly Thr Leu Val Gln Phe Cys Gly Asn Asn 170	175	180	643
GTT TTT GAT CAT TTG AAA GTC AAC GAT AAG TTT GAC AAA AAG CAA AAA Val Phe Asp His Leu Lys Val Asn Asp Lys Phe Asp Lys Lys Gln Lys 185	190	195	691
GGT GGA GCA GCA GAC ATG AAT GAA CCT CGA TGT TGA TCA ACC TGC AAA Gly Gly Ala Ala Asp Met Asn Glu Pro Arg Cys Cys Ser Thr Cys Lys 200	205	210	739
TAC AAT GTC AAG AAT GAG AAA GAT CAC TTT CTC AAC AAC ATC AAC GTG Tyr Asn Val Lys Asn Glu Lys Asp His Phe Leu Asn Asn Ile Asn Val 215	220	225	787
CCG AAT TGG AAT AAT ATG AAA TCA AGA ACC AGA ATA TTT TAT TGC ACT Pro Asn Trp Asn Asn Met Lys Ser Arg Thr Arg Ile Phe Tyr Cys Thr 230	235	240	835
CAT TTT AAT AGA AAT AAC CAA TTC TTC AAA AAG CAT GAG TTT GTG AGT His Phe Asn Arg Asn Asn Gln Phe Phe Lys Lys His Glu Phe Val Ser 250	255	260	883
AAC AAA AAC AAT ATT TCA GCG ATG GAC AGA GCT CAG ACG ATA TTC ACG Asn Lys Asn Asn Ile Ser Ala Met Asp Arg Ala Gln Thr Ile Phe Thr 265	270	275	931

AAT ATA TTC AGA TTT AAT AGA ATT AGA AAG AAG CTA AAA GAT AAG GTT Asn Ile Phe Arg Phe Asn Arg Ile Arg Lys Lys Leu Lys Asp Lys Val 280 285 290	979
ATC GAA AAA ATT GCC TAC ATG CTT GAG AAA GTC AAA GAT TTT AAC TTC Ile Glu Lys Ile Ala Tyr Met Leu Glu Lys Val Lys Asp Phe Asn Phe 295 300 305	1027
AAC TAC TAT TTA ACA AAA TCT TGT CCT CTT CCA GAA AAT TGG CGG GAA Asn Tyr Tyr Leu Thr Lys Ser Cys Pro Leu Pro Glu Asn Trp Arg Glu 310 315 320 325	1075
CGG AAA CAA AAA ATC GAA AAC TTG ATA AAT AAA ACT AGA GAA GAA AAG Arg Lys Gln Lys Ile Glu Asn Leu Ile Asn Lys Thr Arg Glu Glu Lys 330 335 340	1123
TCG AAG TAC TAT GAA GAG CTG TTT AGC TAC ACA ACT GAT AAT AAA TGC Ser Lys Tyr Tyr Glu Glu Leu Phe Ser Tyr Thr Thr Asp Asn Lys Cys 345 350 355	1171
GTC ACA CAA TTT ATT AAT GAA TTT TTC TAC AAT ATA CTC CCC AAA GAC Val Thr Gln Phe Ile Asn Glu Phe Phe Tyr Asn Ile Leu Pro Lys Asp 360 365 370	1219
TTT TTG ACT GGA AGA AAC CGT AAG AAT TTT CAA AAG AAA GTT AAG AAA Phe Leu Thr Gly Arg Asn Arg Lys Asn Phe Gln Lys Lys Val Lys Lys 375 380 385	1267
TAT GTG GAA CTA AAC AAG CAT GAA CTC ATT CAC AAA AAC TTA TTG CTT Tyr Val Glu Leu Asn Lys His Glu Leu Ile His Lys Asn Leu Leu 390 395 400 405	1315
GAG AAG ATC AAT ACA AGA GAA ATA TCA TGG ATG CAG GTT GAG ACC TCT Glu Lys Ile Asn Thr Arg Glu Ile Ser Trp Met Gln Val Glu Thr Ser 410 415 420	1363
GCA AAG CAT TTT TAT TAT TTT GAT CAC GAA AAC ATC TAC GTC TTA TGG Ala Lys His Phe Tyr Tyr Phe Asp His Glu Asn Ile Tyr Val Leu Trp 425 430 435	1411
AAA TTG CTC CGA TGG ATA TTC GAG GAT CTC GTC GTC TCG CTG ATT AGA Lys Leu Leu Arg Trp Ile Phe Glu Asp Leu Val Val Ser Leu Ile Arg 440 445 450	1459
TGA TTT TTC TAT GTC ACC GAG CAA CAG AAA AGT TAC TCC AAA ACC TAT Cys Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr 455 460 465	1507
TAC TAC AGA AAG AAT ATT TGG GAC GTC ATT ATG AAA ATG TCA ATC GCA Tyr Tyr Arg Lys Asn Ile Trp Asp Val Ile Met Lys Met Ser Ile Ala 470 475 480 485	1555
GAC TTA AAG AAG GAA ACG CTT GCT GAG GTC CAA GAA AAA GAG GTT GAA Asp Leu Lys Lys Glu Thr Leu Ala Glu Val Gln Glu Lys Glu Val Glu 490 495 500	1603
GAA TGG AAA AAG TCG CTT GGA TTT GCA CCT GGA AAA CTC AGA CTA ATA Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly Lys Leu Arg Leu Ile 505 510 515	1651

CCG AAG AAA ACT ACT TTC CGT CCA ATT ATG ACT TTC AAT AAG AAG ATT Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr Phe Asn Lys Lys Ile 520 525 530	1699
GTA AAT TCA GAC CGG AAG ACT ACA AAA TTA ACT ACA AAT ACG AAG TTA Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr Thr Asn Thr Lys Leu 535 540 545	1747
TTG AAC TCT CAC TTA ATG CTT AAG ACA TTG AAG AAT AGA ATG TTT AAA Leu Asn Ser His Leu Met Leu Lys Thr Leu Lys Asn Arg Met Phe Lys 550 555 560 565	1795
GAT CCT TTT GGA TTC GCT GTT TTT AAC TAT GAT GAT GTA ATG AAA AAG Asp Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp Asp Val Met Lys Lys 570 575 580	1843
TAT GAG GAG TTT GTT TGC AAA TGG AAG CAA GTT GGA CAA CCA AAA CTC Tyr Glu Glu Phe Val Cys Lys Trp Lys Gln Val Gly Gln Pro Lys Leu 585 590 595	1891
TTC TTT GCA ACT ATG GAT ATC GAA AAG TGA TAT GAT AGT GTA AAC AGA Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp Ser Val Asn Arg 600 605 610	1939
GAA AAA CTA TCA ACA TTC CTA AAA ACT ACT AAA TTA CTT TCT TCA GAT Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys Leu Leu Ser Ser Asp 615 620 625	1987
TTC TGG ATT ATG ACT GCA CAA ATT CTA AAG AGA AAG AAT AAC ATA GTT Phe Trp Ile Met Thr Ala Gln Ile Leu Lys Arg Lys Asn Asn Ile Val 630 635 640 645	2035
ATC GAT TCG AAA AAC TTT AGA AAG AAA GAA ATG AAA GAT TAT TTT AGA Ile Asp Ser Lys Asn Phe Arg Lys Lys Glu Met Lys Asp Tyr Phe Arg 650 655 660	2083
CAG AAA TTC CAG AAG ATT GCA CTT GAA GGA GGA CAA TAT CCA ACC TTA Gln Lys Phe Gln Lys Ile Ala Leu Glu Gly Gly Gln Tyr Pro Thr Leu 665 670 675	2131
TTC AGT GTT CTT GAA AAT GAA CAA AAT GAC TTA AAT GCA AAG AAA ACA Phe Ser Val Leu Glu Asn Glu Gln Asn Asp Leu Asn Ala Lys Lys Thr 680 685 690	2179
TTA ATT GTT GAA GCA AAG CAA AGA AAT TAT TTT AAG AAA GAT AAC TTA Leu Ile Val Glu Ala Lys Gln Arg Asn Tyr Phe Lys Lys Asp Asn Leu 695 700 705	2227
CTT CAA CCA GTC ATT AAT ATT TGC CAA TAT AAT TAC ATT AAC TTT AAT Leu Gln Pro Val Ile Asn Ile Cys Gln Tyr Asn Tyr Ile Asn Phe Asn 710 715 720 725	2275
GGG AAG TTT TAT AAA CAA ACA AAA GGA ATT CCT CAA GGT CTT TGA GTT Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys Val 730 735 740	2323
TCA TCA ATT TTG TCA TCA TTT TAT TAT GCA ACA TTA GAG GAA AGC TCC Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu Glu Ser Ser 745 750 755	2371

TTA GGA TTC CTT AGA GAT GAA TCA ATG AAC CCT GAA AAT CCA AAT GTT Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro Glu Asn Pro Asn Val 760 765 770	2419
AAT CTT CTA ATG AGA CTT ACA GAT GAC TAT CTT TTG ATT ACA ACT CAA Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Ile Thr Thr Gln 775 780 785	2467
GAG AAT AAT GCA GTA TTG TTT ATT GAG AAA CTT ATA AAC GTA AGT CGT Glu Asn Asn Ala Val Leu Phe Ile Glu Lys Leu Ile Asn Val Ser Arg 790 795 800 805	2515
GAA AAT GGA TTT AAA TTC AAT ATG AAG AAA CTA CAG ACT AGT TTT CCA Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu Gln Thr Ser Phe Pro 810 815 820	2563
TTA AGT CCA AGC AAA TTT GCA AAA TAC GGA ATG GAT AGT GTT GAG GAG Leu Ser Pro Ser Lys Phe Ala Lys Tyr Gly Met Asp Ser Val Glu Glu 825 830 835	2611
CAA AAT ATT GTT CAA GAT TAC TGC GAT TGG ATT GGC ATC TCA ATT GAT Gln Asn Ile Val Gln Asp Tyr Cys Asp Trp Ile Gly Ile Ser Ile Asp 840 845 850	2659
ATG AAA ACT CTT GCT TTA ATG CCA AAT ATT AAC TTG AGA ATA GAA GGA Met Lys Thr Leu Ala Leu Met Pro Asn Ile Asn Leu Arg Ile Glu Gly 855 860 865	2707
ATT CTG TGT ACA CTC AAT CTA AAC ATG CAA ACA AAG AAA GCA TCA ATG Ile Leu Cys Thr Leu Asn Leu Asn Met Gln Thr Lys Lys Ala Ser Met 870 875 880 885	2755
TGG CTC AAG AAG AAA CTA AAG TCG TTT TTA ATG AAT AAC ATT ACC CAT Trp Leu Lys Lys Leu Lys Ser Phe Leu Met Asn Asn Ile Thr His 890 895 900	2803
TAT TTT AGA AAG ACG ATT ACA ACC GAA GAC TTT GCG AAT AAA ACT CTC Tyr Phe Arg Lys Thr Ile Thr Glu Asp Phe Ala Asn Lys Thr Leu 905 910 915	2851
AAC AAG TTA TTT ATA TCA GGC GGT TAC AAA TAC ATG CAA TGA GCC AAA Asn Lys Leu Phe Ile Ser Gly Gly Tyr Lys Tyr Met Gln Cys Ala Lys 920 925 930	2899
GAA TAC AAG GAC CAC TTT AAG AAG AAC TTA GCT ATG AGC AGT ATG ATC Glu Tyr Lys Asp His Phe Lys Lys Asn Leu Ala Met Ser Ser Met Ile 935 940 945	2947
GAC TTA GAG GTA TCT AAA ATT ATA TAC TCT GTA ACC AGA GCA TTC TTT Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val Thr Arg Ala Phe Phe 950 955 960 965	2995
AAA TAC CTT GTG TGC AAT ATT AAG GAT ACA ATT TTT GGA GAG GAG CAT Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile Phe Gly Glu Glu His 970 975 980	3043
TAT CCA GAC TTT TTC CTT AGC ACA CTG AAG CAC TTT ATT GAA ATA TTC Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His Phe Ile Glu Ile Phe 985 990 995	3091

AGC ACA AAA AAG TAC ATT TTC AAC AGA GTT TGC ATG ATC CTC AAG GCA Ser Thr Lys Lys Tyr Ile Phe Asn Arg Val Cys Met Ile Leu Lys Ala 1000 1005 1010	3139
AAA GAA GCA AAG CTA AAA AGT GAC CAA TGT CAA TCT CTA ATT CAA TAT Lys Glu Ala Lys Leu Lys Ser Asp Gln Cys Gln Ser Leu Ile Gln Tyr 1015 1020 1025	3187
GAT GCA TAGTCGACTA TTCTAACTTA TTTTGGAAAG TTAATTTCATTTTGCTC Asp Ala 1030	3243
TATATACTGG GGTTTTGGGG TTTTGGGGTT TTGGGG	3279

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1031 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Val Asp Val Asp Asn Gln Ala Asp Asn His Gly Ile His Ser 1 5 10 15
Ala Leu Lys Thr Cys Glu Glu Ile Lys Glu Ala Lys Thr Leu Tyr Ser 20 25 30
Trp Ile Gln Lys Val Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr 35 40 45
Lys Asp Leu Glu Asp Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala 50 55 60
Thr Pro Arg Asp Tyr Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys 65 70 75 80
Glu Val Phe Ser Thr Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu 85 90 95
Val Glu Leu Leu Ser Ser Asp Val Ser Asp Arg Gln Lys Leu Gln 100 105 110
Cys Phe Gly Phe Gln Leu Lys Gly Asn Gln Leu Ala Lys Thr His Leu 115 120 125
Leu Thr Ala Leu Ser Thr Gln Lys Gln Tyr Phe Phe Gln Asp Glu Trp 130 135 140
Asn Gln Val Arg Ala Met Ile Gly Asn Glu Leu Phe Arg His Leu Tyr 145 150 155 160
Thr Lys Tyr Leu Ile Phe Gln Arg Thr Ser Glu Gly Thr Leu Val Gln 165 170 175
Phe Cys Gly Asn Asn Val Phe Asp His Leu Lys Val Asn Asp Lys Phe 180 185 190

Asp Lys Lys Gln Lys Gly Gly Ala Ala Asp Met Asn Glu Pro Arg Cys
 195 200 205
 Cys Ser Thr Cys Lys Tyr Asn Val Lys Asn Glu Lys Asp His Phe Leu
 210 215 220
 Asn Asn Ile Asn Val Pro Asn Trp Asn Asn Met Lys Ser Arg Thr Arg
 225 230 235 240
 Ile Phe Tyr Cys Thr His Phe Asn Arg Asn Asn Gln Phe Phe Lys Lys
 245 250 255
 His Glu Phe Val Ser Asn Lys Asn Ile Ser Ala Met Asp Arg Ala
 260 265 270
 Gln Thr Ile Phe Thr Asn Ile Phe Arg Phe Asn Arg Ile Arg Lys Lys
 275 280 285
 Leu Lys Asp Lys Val Ile Glu Lys Ile Ala Tyr Met Leu Glu Lys Val
 290 295 300
 Lys Asp Phe Asn Phe Asn Tyr Tyr Leu Thr Lys Ser Cys Pro Leu Pro
 305 310 315 320
 Glu Asn Trp Arg Glu Arg Lys Gln Lys Ile Glu Asn Leu Ile Asn Lys
 325 330 335
 Thr Arg Glu Glu Lys Ser Lys Tyr Tyr Glu Glu Leu Phe Ser Tyr Thr
 340 345 350
 Thr Asp Asn Lys Cys Val Thr Gln Phe Ile Asn Glu Phe Phe Tyr Asn
 355 360 365
 Ile Leu Pro Lys Asp Phe Leu Thr Gly Arg Asn Arg Lys Asn Phe Gln
 370 375 380
 Lys Lys Val Lys Lys Tyr Val Glu Leu Asn Lys His Glu Leu Ile His
 385 390 395 400
 Lys Asn Leu Leu Leu Glu Lys Ile Asn Thr Arg Glu Ile Ser Trp Met
 405 410 415
 Gln Val Glu Thr Ser Ala Lys His Phe Tyr Tyr Phe Asp His Glu Asn
 420 425 430
 Ile Tyr Val Leu Trp Lys Leu Leu Arg Trp Ile Phe Glu Asp Leu Val
 435 440 445
 Val Ser Leu Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser
 450 455 460
 Tyr Ser Lys Thr Tyr Tyr Arg Lys Asn Ile Trp Asp Val Ile Met
 465 470 475 480
 Lys Met Ser Ile Ala Asp Leu Lys Lys Glu Thr Leu Ala Glu Val Gln
 485 490 495
 Glu Lys Glu Val Glu Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly
 500 505 510

Lys Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr
 515 520 525
 Phe Asn Lys Lys Ile Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr
 530 535 540
 Thr Asn Thr Lys Leu Leu Asn Ser His Leu Met Leu Lys Thr Leu Lys
 545 550 555 560
 Asn Arg Met Phe Lys Asp Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp
 565 570 575
 Asp Val Met Lys Lys Tyr Glu Glu Phe Val Cys Lys Trp Lys Gln Val
 580 585 590
 Gly Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr
 595 600 605
 Asp Ser Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys
 610 615 620
 Leu Leu Ser Ser Asp Phe Trp Ile Met Thr Ala Gln Ile Leu Lys Arg
 625 630 635 640
 Lys Asn Asn Ile Val Ile Asp Ser Lys Asn Phe Arg Lys Lys Glu Met
 645 650 655
 Lys Asp Tyr Phe Arg Gln Lys Phe Gln Lys Ile Ala Leu Glu Gly Gly
 660 665 670
 Gln Tyr Pro Thr Leu Phe Ser Val Leu Glu Asn Glu Gln Asn Asp Leu
 675 680 685
 Asn Ala Lys Lys Thr Leu Ile Val Glu Ala Lys Gln Arg Asn Tyr Phe
 690 695 700
 Lys Lys Asp Asn Leu Leu Gln Pro Val Ile Asn Ile Cys Gln Tyr Asn
 705 710 715 720
 Tyr Ile Asn Phe Asn Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro
 725 730 735
 Gln Gly Leu Cys Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr
 740 745 750
 Leu Glu Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro
 755 760 765
 Glu Asn Pro Asn Val Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu
 770 775 780
 Leu Ile Thr Thr Gln Glu Asn Asn Ala Val Leu Phe Ile Glu Lys Leu
 785 790 795 800
 Ile Asn Val Ser Arg Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu
 805 810 815
 Gln Thr Ser Phe Pro Leu Ser Pro Ser Lys Phe Ala Lys Tyr Gly Met
 820 825 830

Asp	Ser	Val	Glu	Glu	Gln	Asn	Ile	Val	Gln	Asp	Tyr	Cys	Asp	Trp	Ile
835															845
Gly	Ile	Ser	Ile	Asp	Met	Lys	Thr	Leu	Ala	Leu	Met	Pro	Asn	Ile	Asn
850															860
Leu	Arg	Ile	Glu	Gly	Ile	Leu	Cys	Thr	Leu	Asn	Leu	Asn	Met	Gln	Thr
865															880
Lys	Lys	Ala	Ser	Met	Trp	Leu	Lys	Lys	Lys	Leu	Lys	Ser	Phe	Leu	Met
885															895
Asn	Asn	Ile	Thr	His	Tyr	Phe	Arg	Lys	Thr	Ile	Thr	Thr	Glu	Asp	Phe
900															910
Ala	Asn	Lys	Thr	Leu	Asn	Lys	Leu	Phe	Ile	Ser	Gly	Gly	Tyr	Lys	Tyr
915															925
Met	Gln	Cys	Ala	Lys	Glu	Tyr	Lys	Asp	His	Phe	Lys	Lys	Asn	Leu	Ala
930															940
Met	Ser	Ser	Met	Ile	Asp	Leu	Glu	Val	Ser	Lys	Ile	Ile	Tyr	Ser	Val
945															960
Thr	Arg	Ala	Phe	Phe	Lys	Tyr	Leu	Val	Cys	Asn	Ile	Lys	Asp	Thr	Ile
965															975
Phe	Gly	Glu	Glu	His	Tyr	Pro	Asp	Phe	Phe	Leu	Ser	Thr	Leu	Lys	His
980															990
Phe	Ile	Glu	Ile	Phe	Ser	Thr	Lys	Lys	Tyr	Ile	Phe	Asn	Arg	Val	Cys
995															1005
Met	Ile	Leu	Lys	Ala	Lys	Glu	Ala	Lys	Leu	Lys	Ser	Asp	Gln	Cys	Gln
1010															1020
Ser	Leu	Ile	Gln	Tyr	Asp	Ala									
1025															1030

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1762 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1762
 - (D) OTHER INFORMATION: /note= "DNA encoding three open reading frames (ORF) for Euplotes aediculatus 43 kD telomerase protein subunit given in SEQ ID NOS:4-6"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCCAAAACC CCAAAACCCC AAAACCCCTA TAAAAAAAGA AAAAATTGAG GTAGTTAGA	60
AATAAAATAT TATTCCCGCA CAAATGGAGA TGGATATTGA TTTGGATGAT ATAGAAAATT	120
TACTTCCTAA TACATTCAAC AAGTATAGCA GCTCTTGTAG TGACAAGAAA GGATGCAAAA	180
CATTGAAATC TGGCTCGAAA TCGCCTTCAT TGACTATTCC AAAGTTGCAA AAACAATTAG	240
AGTTCTACTT CTCGGATGCA AATCTTTATA ACGATTCTT CTTGAGAAAA TTAGTTTAA	300
AAAGCGGAGA GCAAAGAGTA GAAATTGAAA CATTACTAAT GTTTAAATAA AATCAGGTAA	360
TGAGGATTAT TCTATTTTT AGATCACTTC TTAAGGAGCA TTATGGAGAA AATTACTTAA	420
TACTAAAAGG TAAACAGTTT GGATTATTTC CCTAGCCAAC AATGATGAGT ATATTAAATT	480
CATATGAGAA TGAGTCAAAG GATCTCGATA CATCAGACTT ACCAAAGACA AACTCGCTAT	540
AAAACGCAAG AAAAAGTTG ATAATCGAAC AGCAGAAGAA CTTATTGCAT TTACTATTCG	600
TATGGGTTTT ATTACAATTG TTTTAGGTAT CGACGGTGAA CTCCCGAGTC TTGAGACAAT	660
TGAAAAGCT GTTTACAAC GAAGGAATCG CAGTTCTGAA AGTTCTGATG TGTATGCCAT	720
TATTTGTGA ATTAATCTCA AATATCTTAT CTCATTAA TGGATAGCTA TAGAAACAAA	780
CCAAATAAAC CATGCAAGTT TAATGGAATA TACGTTAAAT CCTTTGGGAC AAATGCACAC	840
TGAATTTATA TTGGATTCTT AAAGCATAGA TACACAGAAT GCTTAGAGA CTGATTTAGC	900
TTACAACAGA TTACCTGTT TGATTACTCT TGCTCATCTC TTATATCTT AAAAGAAGCA	960
GGCGAAATGA AAAGAAGACT AAAGAAAGAG ATTCAAAAT TTGTTGATTC TTCTGTAACC	1020
GGAATTAACA ACAAGAATAT TAGCAACGAA AAAGAAGAAG AGCTATCACA ATCCTGATTG	1080
TTAAAGATT CAAAAATTCC AGGTAAGAGA GATACATTCA TTAAATTCA TATATTATAG	1140
TTTTCATTT CACAGCTGTT ATTTCTTTT ATCTTAACAA TATTTTGAA TTAGCTGGAA	1200
GTAAAAAGTA TCAAATAAGA GAAGCGCTAG ACTGAGGTAA CTTAGCTTAT TCACATTCT	1260
AGATCGACCT TCATATATCC AATACGATGA TAAGGAAACA GCAGTCATCC GTTTAAAAAA	1320
TAGTGCTATG AGGACTAAAT TTTTAGAGTC AAGAAATGGA GCCGAAATCT TAATCAAAAA	1380
GAATTGCGTC GATATTGCAA AAGAATCGAA CTCTAAATCT TTCGTTAATA AGTATTACCA	1440
ATCTTGATTG ATTGAAGAGA TTGACGAGGC AACTGCACAG AAGATCATT AAGAAATAAA	1500
GTAACCTTTA TTAATTAGAG AATAAACTAA ATTACTAATA TAGAGATCAG CGATCTCAA	1560
TTGACGAAAT AAAAGCTGAA CTAAAGTTAG ACAATAAAAA ATACAAACCT TGGTCAAAAT	1620
ATTGAGGAAG GAAAAGAAGA CCAGTTAGCA AAAGAAAAAA TAAGGCAATA AATAAAATGA	1680
GTACAGAAGT GAAGAAATAA AAGATTATT TTTTCAATA ATTTATTGAA AAGAGGGTT	1740
TTGGGGTTTT GGGTTTTGG GG	1762

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1040 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..300
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 1-300 may be present or absent"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 630
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at position 630 may be present or absent"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 649..663
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 649-663 may be present or absent"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 674..688
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 674-688 may be present or absent"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 701..706
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 701-706 may be present or absent"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 771..790
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 771-790 may be present or absent"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 887..937
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 887-937 may be present or absent"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 965..994
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 965-994 may be
present or absent"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 1018..1027
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 1018-1027 may
be present or absent"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Xaa
1 5 10 15

Xaa
20 25 30

Xaa
35 40 45

Xaa
50 55 60

Xaa
65 70 75 80

Xaa
85 90 95

Xaa
100 105 110

Xaa
115 120 125

Xaa
130 135 140

Xaa
145 150 155 160

Xaa
165 170 175

Xaa
180 185 190

Xaa
195 200 205

Xaa
210 215 220

Xaa
225 230 235 240

Xaa		
245	250	255
Xaa		
260	265	270
Xaa		
275	280	285
Xaa		
290	295	300
Xaa		
305	310	315
Xaa		
325	330	335
Xaa		
340	345	350
Xaa		
355	360	365
Xaa		
370	375	380
Xaa		
385	390	395
Xaa		
405	410	415
Xaa		
420	425	430
Xaa		
435	440	445
Xaa		
450	455	460
Xaa		
465	470	475
Xaa		
485	490	495
Xaa		
500	505	510
Xaa		
515	520	525
Xaa		
530	535	540
Xaa		
545	550	555
		560

Xaa		
565	570	575
Xaa		
580	585	590
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa		
595	600	605
Xaa Xaa Xaa Xaa Xaa Phe Phe Tyr Xaa Thr Glu Xaa Xaa Xaa Xaa Xaa Xaa		
610	615	620
Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa Xaa Trp Xaa Xaa Xaa Xaa Xaa Xaa		
625	630	635
Xaa Xaa Ile Xaa		
645	650	655
Xaa Xaa Xaa Xaa Xaa Xaa Glu Xaa Xaa Val Xaa Xaa Xaa Xaa Xaa Xaa		
660	665	670
Xaa		
675	680	685
Xaa Xaa Xaa Arg Xaa Xaa Pro Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa		
690	695	700
Xaa Xaa Arg Xaa Ile Xaa		
705	710	720
Xaa		
725	730	735
Xaa		
740	745	750
Xaa		
755	760	765
Xaa		
770	775	780
Xaa Phe Xaa Xaa Xaa Asp Xaa		
785	790	800
Xaa Xaa Xaa Tyr Asp Xaa		
805	810	815
Xaa		
820	825	830
Xaa		
835	840	845
Xaa		
850	855	860
Xaa		
865	870	875
		880

Xaa		
885	890	895
Xaa		
900	905	910
Xaa		
915	920	925
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Xaa Xaa Xaa Gly Xaa		
930	935	940
Xaa Gln Gly Xaa Xaa Xaa Ser Xaa		
945	950	955
Xaa		
965	970	975
Xaa		
980	985	990
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Asp Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa		
995	1000	1005
Xaa		
1010	1015	1020
Xaa Lys		
1025	1030	1035
		1040

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCCCGGATCC TGCGCATGTG TGAGCCGAGT CCTGGG

36

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Leu Val Asp Asp Phe Leu
1 5

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Trp Xaa Gly Xaa Ser Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 1
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 6
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Xaa Leu Gly Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asp	Ile	Asp	Leu	Asp	Asp	Ile	Glu	Asn	Leu	Leu	Pro	Asn	Thr	Phe	Asn
1						5					10				15
Lys	Tyr	Ser	Ser	Ser	Cys	Ser	Asp	Lys	Lys	Gly	Cys	Lys	Thr	Leu	Lys
						20				25				30	
Ser	Gly	Ser	Lys	Ser	Pro	Ser	Leu	Thr	Ile	Pro	Lys	Leu	Gln	Lys	Gln
						35				40				45	
Leu	Glu	Phe	Tyr	Phe	Ser	Asp	Ala	Asn	Leu	Tyr	Asn	Asp	Ser	Phe	Leu
						50				55				60	
Arg	Lys	Leu	Val	Leu	Lys	Ser	Gly	Glu	Gln	Arg	Val	Glu	Ile	Glu	Thr
						65				70				75	
Leu	Leu	Met													80

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Asn	Val	Lys	Ser	Ala	Lys	Ile	Glu	Ser	Ser	Leu	Glu	Ser	Leu	Glu	
1						5				10				15	
Asp	Ile	Asp	Ser	Leu	Cys	Lys	Ser	Ile	Ala	Ser	Cys	Lys	Asn	Leu	Gln
						20				25				30	
Asn	Val	Asn	Ile	Ile	Ala	Ser	Leu	Leu	Tyr	Pro	Asn	Asn	Ile	Gln	Lys
						35				40				45	
Asn	Pro	Phe	Asn	Lys	Pro	Asn	Leu	Leu	Phe	Phe	Lys	Gln	Phe	Glu	Gln
						50				55				60	
Leu	Lys	Asn	Leu	Glu	Asn	Val	Ser	Ile	Asn	Cys	Ile	Leu	Asp	Gln	His
						65				70				75	
Ile	Leu	Asn	Ser	Ile	Ser	Glu	Phe	Leu	Glu	Lys	Asn	Lys	Lys	Ile	Lys
						85				90				95	

Ala Phe Ile Leu
100

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Glu	Met	Asp	Ile	Asp	Leu	Asp	Asp	Ile	Glu	Asn	Leu	Leu	Pro	Asn
1				5					10					15	
Thr	Phe	Asn	Lys	Tyr	Ser	Ser	Ser	Cys	Ser	Asp	Lys	Lys	Gly	Cys	Lys
				20				25					30		
Thr	Leu	Lys	Ser	Gly	Ser	Lys	Ser	Pro	Ser	Leu	Thr	Ile	Pro	Lys	Leu
				35				40				45			
Gln	Lys	Gln	Leu	Glu	Phe	Tyr	Phe	Ser	Asp	Ala	Asn	Leu	Tyr	Asn	Asp
				50			55				60				
Ser	Phe	Leu	Arg	Lys	Leu	Val	Leu	Lys	Ser	Gly	Glu	Gln	Arg	Val	Glu
				65			70			75		80			
Ile	Glu	Thr	Leu	Leu											
				85											

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 99 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ile	Glu	Leu	Ala	Ile	Lys	Ile	Ala	Val	Asn	Lys	Asn	Leu	Asp	Glu	Ile
1				5					10				15		
Lys	Gly	His	Thr	Ala	Ile	Phe	Ser	Asp	Val	Ser	Gly	Ser	Met	Ser	Thr
				20				25					30		
Ser	Met	Ser	Gly	Gly	Ala	Lys	Lys	Tyr	Gly	Ser	Val	Arg	Thr	Cys	Leu
				35				40				45			
Glu	Cys	Ala	Leu	Val	Leu	Gly	Leu	Met	Val	Lys	Gln	Arg	Cys	Glu	Lys
				50			55			60					

Ser Ser Phe Tyr Ile Phe Ser Ser Pro Ser Ser Gln Cys Asn Lys Cys
65 70 75 80
Tyr Leu Glu Val Asp Leu Pro Gly Asp Glu Leu Arg Pro Ser Met Gln
85 90 95
Lys Leu Leu

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Xaa Xaa Asp Asp Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Val"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 5
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Xaa Xaa Asp Asp Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 1
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 5
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Xaa Xaa Asp Asp Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 2
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 10
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 11
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 12
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Gln or Arg"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 28
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 29
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 31
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Lys or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Trp Xaa Phe Phe Trp
1 5 10 15

Xaa Thr Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa
20 25 30

Xaa Trp

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 2
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 10
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 11
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 12
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Gln or Arg"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 29
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 30
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 32
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Lys or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Trp	Xaa	Phe	Phe	Trp										
1														15
Xaa	Thr	Glu	Xaa	Arg	Xaa									
														30
Xaa	Xaa	Trp												
		35												

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 2
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 7..8
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 10..11
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 12
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Gln or Arg"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 13
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid,
selected from Gly, Ser, Thr, Tyr, Cys,
Asn or Gln"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 21
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid,
selected from Gly, Ser, Thr, Tyr, Cys,
Asn or Gln"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 25
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid,
selected from Gly, Ser, Thr, Tyr, Cys,
Asn or Gln"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 28..29
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 31
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Lys or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Trp	Xaa	Phe	Phe	Tyr										
1												10		15
	Xaa	Thr	Glu	Xaa	Arg	Xaa	Xaa							
												25		30
	Xaa	Trp												

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 2
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 7..8
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 10..11
(D) OTHER INFORMATION: /product= "OTHER"

/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 12
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Gln or Arg"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 13
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid,
selected from Gly, Ser, Thr, Tyr, Cys,
Asn or Gln"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 21
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid,
selected from Gly, Ser, Thr, Tyr, Cys,
Asn or Gln"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 25
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid,
selected from Gly, Ser, Thr, Tyr, Cys,
Asn or Gln"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 29..30
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 32
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Lys or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Trp	Xaa	Phe	Phe	Tyr										
1														15
Xaa	Thr	Glu	Xaa	Arg	Xaa									
														30
Xaa	Xaa	Trp												
		35												

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Gly Ser Val Thr Lys
1 5

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Asn Ser Ala Val Asp
1 5

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTTCAAGACC ATCCTGGACT TTCGAAACGC GGCGGCCACC GCGGTGGAGC TCC

53

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Leu	Gln	Lys	Gln	Leu	Glu	Phe	Tyr	Phe	Ser	Asp	Ala	Asn	Leu	Tyr	Asn
1				5					10					15	
Asp	Ser	Phe	Leu	Arg	Lys	Leu	Val	Leu	Lys	Ser	Gly	Glu	Gln	Arg	Val
			20					25					30		
Glu	Ile	Glu	Thr	Leu	Leu	Met									
			35												

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ile	Cys	His	Gln	Xaa	Glu	Tyr	Tyr	Phe	Gly	Asp	Phe	Asn	Leu	Pro	Arg
1					5				10					15	
Asp	Lys	Phe	Leu	Lys	Glu	Gln	Ile	Lys	Leu	Asp	Glu	Gly	Trp	Val	Pro
			20					25					30		
Leu	Glu	Ile	Met	Ile	Lys										
			35												

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ile	Cys	Glu	Gln	Ile	Glu	Tyr	Tyr	Phe	Gly	Asp	His	Asn	Leu	Pro	Arg
1					5				10					15	
Asp	Lys	Phe	Leu	Lys	Gln	Gln	Ile	Leu	Leu	Asp	Asp	Gly	Trp	Val	Pro
			20					25					30		
Leu	Glu	Thr	Met	Ile	Lys										
			35												

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Ile	Leu	Arg	Gln	Val	Glu	Tyr	Tyr	Phe	Gly	Asp	Ala	Asn	Leu	Asn	Arg
1				5					10					15	
Asp	Lys	Phe	Leu	Arg	Glu	Gln	Ile	Gly	Lys	Asn	Glu	Asp	Gly	Trp	Val
			20					25					30		
Pro	Leu	Ser	Val	Leu	Val	Thr									
			35												

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Cys	Leu	Lys	Gln	Val	Glu	Phe	Tyr	Phe	Ser	Glu	Phe	Asn	Phe	Pro	Tyr
1				5					10					15	
Asp	Arg	Phe	Leu	Arg	Thr	Thr	Ala	Glu	Lys	Asn	Asp	Gly	Trp	Val	Pro
			20				25					30			
Ile	Ser	Thr	Ile	Ala	Thr										
			35												

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TAGACCTGTT AGTGTACATT TGAATTGAAG C

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TAGACCTGTT AGGTTGGATT TGTGGCATCA

30

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CAAAACCCCA AAACCTAACCA GGTCTA

26

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCAGGAATTC TAATACGACT CACTATAGGG AAGAAACTCT GATGAGGCCG AAAGGCCGAA

60

ACTCCACGAA AGTGGAGTAA GTTTCTCGAT AATTGATCTG TAG

103

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CGGGGATCCT CTTCAAAAGA TGAGAGGACA GCAAAC

36

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CCCCAAAACC CCAAAACCCC AAAACCCCCA CAGGGTTTT GGGGTTTGG GGTTTGGGG

60

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CCAAAACCCC AAAACCCCAA AACCCCCACA GGGGTTTGG GGTTTGGGG TTTTGGGG

58

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AAAACCCCAA AACCCCAAAA CCCCCACAGG GGTTTGGGG TTTTGGGGTT TTGGGG

56

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

AACCCCAAAA CCCCAAAACC CCCACAGGGG TTTTGGGGTT TTGGGGTTTT GGGG

54

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CCCCAAACCC CCAAAACCCC CACAGGGGTT TTGGGGTTTT GGGGTTTT

48

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AAAACCCCAA AACCCCAAAA CCCCCACAGG GGTTTGAGGG TTTTGGGGTT TT

52

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AACCCCAAAA CCCCAAAACC CCCACAGGGG TTTTGGGGTT TTGGGGTTTT

50

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GGGGAAGCTT TAATACGACT CACTATAGGG TTGCGGAGGG TGGGCCTG

48

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CAAAACCCC AAAACCCCCA CAGGGGTTTT GGGGTTTTGG GGTGGG

46

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

AAAACCCCAA AACCCCCACA GGGGTTTTGG GGTTTTGGGG TTTT

44

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CAAAACCCCA AAACC

15

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TTTGCCCC

8

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GGGGTTTT

8

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Arg Phe Ile Pro Lys Pro
1 5

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

TCTRAARTAR TGDGTNADRT TRTTCAT

27

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GCGGATCCAT GAAYCCWGAR AAYCCWAAYG T

31

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

NNNGTNACHG GHATHAAYAA

20

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

DGCDGTYTCY TGRTCRTT A

21

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 92..2251
- (D) OTHER INFORMATION: /codon= (seq: "taa", aa: Gln)
/seq: "tag", aa: Gln
/note= "Tetrahymena thermophila 80 kD
TRT protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

AACTCATTAA	ATTACTAATT	TAATCAACAA	GATTGATAAA	AAGCAGTAAA	TAAAACCCAA	60									
TAGATTTAAT TTAGAAAGTA TCAATTGAAA A ATG GAA ATT GAA AAC AAC TAA						112									
			Met	Glu	Ile	Glu	Asn	Asn	Gln						
			1			5									
GCA CAA TAG CCA AAA GCC GAA AAA TTG TGG TGG GAA CTT GAA TTA GAG						160									
Ala	Gln	Pro	Lys	Ala	Glu	Lys	Leu	Trp	Trp	Glu	Leu	Glu			
10				15						20					
ATG CAA GAA AAC CAA AAT GAT ATA TAA GTT AGG GTT AAG ATT GAC GAT						208									
Met	Gln	Glu	Asn	Gln	Asn	Asp	Ile	Gln	Val	Arg	Val	Lys	Ile	Asp	Asp
25				30					35						
CCT AAG CAA TAT CTC GTG AAC GTC ACT GCA GCA TGT TTG TTG TAG GAA						256									
Pro	Lys	Gln	Tyr	Leu	Val	Asn	Val	Thr	Ala	Ala	Cys	Leu	Leu	Gln	Glu
40				45					50			55			
GGT AGT TAC TAC TAA GAT AAA GAT GAA AGA AGA TAT ATC ATC ACT AAA						304									
Gly	Ser	Tyr	Tyr	Gln	Asp	Lys	Asp	Glu	Arg	Arg	Tyr	Ile	Ile	Thr	Lys
60				65					70						
GCA CTT CTT GAG GTG GCT GAG TCT GAT CCT GAG TTC ATC TGC TAG TTG						352									
Ala	Leu	Glu	Val	Ala	Glu	Ser	Asp	Pro	Glu	Phe	Ile	Cys	Gln	Leu	
75				80					85						
GCA GTC TAC ATC CGT AAT GAA CTT TAC ATC AGA ACT ACC ACT AAC TAC						400									
Ala	Val	Tyr	Ile	Arg	Asn	Glu	Leu	Tyr	Ile	Arg	Thr	Thr	Asn	Tyr	
90				95					100						
ATT GTA GCA TTT TGT GTT GTC CAC AAG AAT ACT CAA CCA TTC ATC GAA						448									
Ile	Val	Ala	Phe	Cys	Val	Val	His	Lys	Asn	Thr	Gln	Pro	Phe	Ile	Glu
105				110					115						
AAG TAC TTC AAC AAA GCA GTC CTT TTG CCT AAT GAC TTA CTG GAA GTC						496									
Lys	Tyr	Phe	Asn	Lys	Ala	Val	Leu	Leu	Pro	Asn	Asp	Leu	Leu	Glu	Val
120				125					130			135			

TGT GAA TTT GCA TAG GTT CTC TAT ATT TTT GAT GCA ACT GAA TTC AAA Cys Glu Phe Ala Gln Val Leu Tyr Ile Phe Asp Ala Thr Glu Phe Lys 140 145 150	544
AAT TTG TAT CTT GAT AGG ATA CTT TCA TAA GAT ATT CGT AAG GAA CTC Asn Leu Tyr Leu Asp Arg Ile Leu Ser Gln Asp Ile Arg Lys Glu Leu 155 160 165	592
ACT TTC CGT AAG TGT TTA CAA AGA TGC GTC AGA AGC AAG TTT TCT GAA Thr Phe Arg Lys Cys Leu Gln Arg Cys Val Arg Ser Lys Phe Ser Glu 170 175 180	640
TTG AAC GAA TAC TAA CTT GGT AAG TAT TGC ACT GAA TCC TAA CGT AAG Phe Asn Glu Tyr Gln Leu Gly Lys Tyr Cys Thr Glu Ser Gln Arg Lys 185 190 195	688
AAA ACA ATG TTC CGT TAC CTC TCA GTT ACC AAC AAG TAA AAG TGG GAT Lys Thr Met Phe Arg Tyr Leu Ser Val Thr Asn Lys Gln Lys Trp Asp 200 205 210 215	736
TAA ACT AAG AAG AAG AGA AAA GAG AAT CTC TTA ACC AAA CTT TAG GCA Gln Thr Lys Lys Arg Lys Glu Asn Leu Leu Thr Lys Leu Gln Ala 220 225 230	784
ATA AAG GAA TCT GAA GAT AAG TCC AAG AGA GAA ACT GGA GAC ATA ATG Ile Lys Glu Ser Glu Asp Lys Ser Lys Arg Glu Thr Gly Asp Ile Met 235 240 245	832
AAC GTT GAA GAT GCA ATC AAG GCT TTA AAA CCA GCA GTT ATG AAG AAA Asn Val Glu Asp Ala Ile Lys Ala Leu Lys Pro Ala Val Met Lys Lys 250 255 260	880
ATA GCC AAG AGA TAG AAT GCC ATG AAG AAA CAC ATG AAG GCA CCT AAA Ile Ala Lys Arg Gln Asn Ala Met Lys Lys His Met Lys Ala Pro Lys 265 270 275	928
ATT CCT AAC TCT ACC TTG GAA TCA AAG TAC TTG ACC TTC AAG GAT CTC Ile Pro Asn Ser Thr Leu Glu Ser Lys Tyr Leu Thr Phe Lys Asp Leu 280 285 290 295	976
ATT AAG TTC TGC CAT ATT TCT GAG CCT AAA GAA AGA GTC TAT AAG ATC Ile Lys Phe Cys His Ile Ser Glu Pro Lys Glu Arg Val Tyr Lys Ile 300 305 310	1024
CTT GGT AAA AAA TAC CCT AAG ACC GAA GAG GAA TAC AAA GCA GCC TTT Leu Gly Lys Tyr Pro Lys Thr Glu Glu Tyr Lys Ala Ala Phe 315 320 325	1072
GGT GAT TCT GCA TCT GCA CCC TTC AAT CCT GAA TTG GCT GGA AAG CGT Gly Asp Ser Ala Ser Ala Pro Phe Asn Pro Glu Leu Ala Gly Lys Arg 330 335 340	1120
ATG AAG ATT GAA ATC TCT AAA ACA TGG GAA AAT GAA CTC AGT GCA AAA Met Lys Ile Glu Ile Ser Lys Thr Trp Glu Asn Glu Leu Ser Ala Lys 345 350 355	1168
GGC AAC ACT GCT GAG GTT TGG GAT AAT TTA ATT TCA AGC AAT TAA CTC Gly Asn Thr Ala Glu Val Trp Asp Asn Leu Ile Ser Ser Asn Gln Leu 360 365 370 375	1216

CCA TAT ATG GCC ATG TTA CGT AAC TTG TCT AAC ATC TTA AAA GCC GGT Pro Tyr Met Ala Met Leu Arg Asn Leu Ser Asn Ile Leu Lys Ala Gly 380 385 390	1264
GTT TCA GAT ACT ACA CAC TCT ATT GTG ATC AAC AAG ATT TGT GAG CCC Val Ser Asp Thr Thr His Ser Ile Val Ile Asn Lys Ile Cys Glu Pro 395 400 405	1312
AAG GCC GTT GAG AAC TCC AAG ATG TTC CCT CTT CAA TTC TTT AGT GCC Lys Ala Val Glu Asn Ser Lys Met Phe Pro Leu Gln Phe Phe Ser Ala 410 415 420	1360
ATT GAA GCT GTT AAT GAA GCA GTT ACT AAG GGA TTC AAG GCC AAG AAG Ile Glu Ala Val Asn Glu Ala Val Thr Lys Gly Phe Lys Ala Lys Lys 425 430 435	1408
AGA GAA AAT ATG AAT CTT AAA GGT CAA ATC GAA GCA GTA AAG GAA GTT Arg Glu Asn Met Asn Leu Lys Gly Gln Ile Glu Ala Val Lys Glu Val 440 445 450 455	1456
GTT GAA AAA ACC GAT GAA GAG AAG AAA GAT ATG GAG TTG GAG TAA ACC Val Glu Lys Thr Asp Glu Glu Lys Lys Asp Met Glu Leu Glu Gln Thr 460 465 470	1504
GAA GAA GGA GAA TTT GTT AAA GTC AAC GAA GGA ATT GCC AAG CAA TAC Glu Glu Gly Glu Phe Val Lys Val Asn Glu Gly Ile Gly Lys Gln Tyr 475 480 485	1552
ATT AAC TCC ATT GAA CTT GCA ATC AAG ATA GCA GTT AAC AAG AAT TTA Ile Asn Ser Ile Glu Leu Ala Ile Lys Ile Ala Val Asn Lys Asn Leu 490 495 500	1600
GAT GAA ATC AAA GGA CAC ACT GCA ATC TTC TCT GAT GTT TCT GGT TCT Asp Glu Ile Lys Gly His Thr Ala Ile Phe Ser Asp Val Ser Gly Ser 505 510 515	1648
ATG AGT ACC TCA ATG TCA GGT GGA GCC AAG AAG TAT GGT TCC GTT CGT Met Ser Thr Ser Met Ser Gly Gly Ala Lys Lys Tyr Gly Ser Val Arg 520 525 530 535	1696
ACT TGT CTC GAG TGT GCA TTA GTC CTT GGT TTG ATG GTA AAA TAA CGT Thr Cys Leu Glu Cys Ala Leu Val Leu Gly Leu Met Val Lys Gln Arg 540 545 550	1744
TGT GAA AAG TCC TCA TTC TAC ATC TTC AGT TCA CCT AGT TCT CAA TGC Cys Glu Lys Ser Ser Phe Tyr Ile Phe Ser Ser Pro Ser Ser Gln Cys 555 560 565	1792
AAT AAG TGT TAC TTA GAA GTT GAT CTC CCT GGA GAC GAA CTC CGT CCT Asn Lys Cys Tyr Leu Glu Val Asp Leu Pro Gly Asp Glu Leu Arg Pro 570 575 580	1840
TCT ATG TAA AAA CTT TTG CAA GAG AAA GGA AAA CTT GGT GGT GGT ACT Ser Met Gln Lys Leu Leu Gln Glu Lys Gly Lys Leu Gly Gly Gly Thr 585 590 595	1888
GAT TTC CCC TAT GAG TGC ATT GAT GAA TGG ACA AAG AAT AAA ACT CAC Asp Phe Pro Tyr Glu Cys Ile Asp Glu Trp Thr Lys Asn Lys Thr His 600 605 610 615	1936

GTA GAC AAT ATC GTT ATT TTG TCT GAT ATG ATG ATT GCA GAA GGA TAT Val Asp Asn Ile Val Ile Leu Ser Asp Met Met Ile Ala Glu Gly Tyr 620 625 630	1984
TCA GAT ATC AAT GTT AGA GGC AGT TCC ATT GTT AAC AGC ATC AAA AAG Ser Asp Ile Asn Val Arg Gly Ser Ser Ile Val Asn Ser Ile Lys Lys 635 640 645	2032
TAC AAG GAT GAA GTA AAT CCT AAC ATT AAA ATC TTT GCA GTT GAC TTA Tyr Lys Asp Glu Val Asn Pro Asn Ile Lys Ile Phe Ala Val Asp Leu 650 655 660	2080
GAA GGT TAC GGA AAG TGC CTT AAT CTA GGT GAT GAG TTC AAT GAA AAC Glu Gly Tyr Gly Lys Cys Leu Asn Leu Gly Asp Glu Phe Asn Glu Asn 665 670 675	2128
AAC TAC ATC AAG ATA TTC GGT ATG AGC GAT TCA ATC TTA AAG TTC ATT Asn Tyr Ile Lys Ile Phe Gly Met Ser Asp Ser Ile Leu Lys Phe Ile 680 685 690 695	2176
TCA GCC AAG CAA GGA GGA GCA AAT ATG GTC GAA GTT ATC AAA AAC TTT Ser Ala Lys Gln Gly Ala Asn Met Val Glu Val Ile Lys Asn Phe 700 705 710	2224
GCC CTT CAA AAA ATA GGA CAA AAG TGAGTTTCTT GAGATTCTTC TATAACAAAA Ala Leu Gln Lys Ile Gly Gln Lys 715	2278
ATCTCACCCCC ACTTTTTGT TTTATTGCAT AGCCATTATG AAATTAAAT TATTATCTAT	2338
TTATTTAAGT TACTTACATA GTTTATGTAT CGCAGTCTAT TAGCCTATTC AAATGATTCT	2398
GCAAAGAACAA AAAAAGATTA AAA	2421

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Glu Ile Glu Asn Asn Gln Ala Gln Gln Pro Lys Ala Glu Lys Leu 1 5 10 15
Trp Trp Glu Leu Glu Met Gln Glu Asn Gln Asn Asp Ile Gln 20 25 30
Val Arg Val Lys Ile Asp Asp Pro Lys Gln Tyr Leu Val Asn Val Thr 35 40 45
Ala Ala Cys Leu Leu Gln Glu Gly Ser Tyr Tyr Gln Asp Lys Asp Glu 50 55 60
Arg Arg Tyr Ile Ile Thr Lys Ala Leu Leu Glu Val Ala Glu Ser Asp 65 70 75 80

Pro Glu Phe Ile Cys Gln Leu Ala Val Tyr Ile Arg Asn Glu Leu Tyr
 85 90 95
 Ile Arg Thr Thr Asn Tyr Ile Val Ala Phe Cys Val Val His Lys
 100 105 110
 Asn Thr Gln Pro Phe Ile Glu Lys Tyr Phe Asn Lys Ala Val Leu Leu
 115 120 125
 Pro Asn Asp Leu Leu Glu Val Cys Glu Phe Ala Gln Val Leu Tyr Ile
 130 135 140
 Phe Asp Ala Thr Glu Phe Lys Asn Leu Tyr Leu Asp Arg Ile Leu Ser
 145 150 155 160
 Gln Asp Ile Arg Lys Glu Leu Thr Phe Arg Lys Cys Leu Gln Arg Cys
 165 170 175
 Val Arg Ser Lys Phe Ser Glu Phe Asn Glu Tyr Gln Leu Gly Lys Tyr
 180 185 190
 Cys Thr Glu Ser Gln Arg Lys Lys Thr Met Phe Arg Tyr Leu Ser Val
 195 200 205
 Thr Asn Lys Gln Lys Trp Asp Gln Thr Lys Lys Lys Arg Lys Glu Asn
 210 215 220
 Leu Leu Thr Lys Leu Gln Ala Ile Lys Glu Ser Glu Asp Lys Ser Lys
 225 230 235 240
 Arg Glu Thr Gly Asp Ile Met Asn Val Glu Asp Ala Ile Lys Ala Leu
 245 250 255
 Lys Pro Ala Val Met Lys Lys Ile Ala Lys Arg Gln Asn Ala Met Lys
 260 265 270
 Lys His Met Lys Ala Pro Lys Ile Pro Asn Ser Thr Leu Glu Ser Lys
 275 280 285
 Tyr Leu Thr Phe Lys Asp Leu Ile Lys Phe Cys His Ile Ser Glu Pro
 290 295 300
 Lys Glu Arg Val Tyr Lys Ile Leu Gly Lys Lys Tyr Pro Lys Thr Glu
 305 310 315 320
 Glu Glu Tyr Lys Ala Ala Phe Gly Asp Ser Ala Ser Ala Pro Phe Asn
 325 330 335
 Pro Glu Leu Ala Gly Lys Arg Met Lys Ile Glu Ile Ser Lys Thr Trp
 340 345 350
 Glu Asn Glu Leu Ser Ala Lys Gly Asn Thr Ala Glu Val Trp Asp Asn
 355 360 365
 Leu Ile Ser Ser Asn Gln Leu Pro Tyr Met Ala Met Leu Arg Asn Leu
 370 375 380
 Ser Asn Ile Leu Lys Ala Gly Val Ser Asp Thr Thr His Ser Ile Val
 385 390 395 400

Ile Asn Lys Ile Cys Glu Pro Lys Ala Val Glu Asn Ser Lys Met Phe
 405 410 415
 Pro Leu Gln Phe Phe Ser Ala Ile Glu Ala Val Asn Glu Ala Val Thr
 420 425 430
 Lys Gly Phe Lys Ala Lys Lys Arg Glu Asn Met Asn Leu Lys Gly Gln
 435 440 445
 Ile Glu Ala Val Lys Glu Val Val Glu Lys Thr Asp Glu Glu Lys Lys
 450 455 460
 Asp Met Glu Leu Glu Gln Thr Glu Glu Gly Glu Phe Val Lys Val Asn
 465 470 475 480
 Glu Gly Ile Gly Lys Gln Tyr Ile Asn Ser Ile Glu Leu Ala Ile Lys
 485 490 495
 Ile Ala Val Asn Lys Asn Leu Asp Glu Ile Lys Gly His Thr Ala Ile
 500 505 510
 Phe Ser Asp Val Ser Gly Ser Met Ser Thr Ser Met Ser Gly Gly Ala
 515 520 525
 Lys Lys Tyr Gly Ser Val Arg Thr Cys Leu Glu Cys Ala Leu Val Leu
 530 535 540
 Gly Leu Met Val Lys Gln Arg Cys Glu Lys Ser Ser Phe Tyr Ile Phe
 545 550 555 560
 Ser Ser Pro Ser Ser Gln Cys Asn Lys Cys Tyr Leu Glu Val Asp Leu
 565 570 575
 Pro Gly Asp Glu Leu Arg Pro Ser Met Gln Lys Leu Leu Gln Glu Lys
 580 585 590
 Gly Lys Leu Gly Gly Thr Asp Phe Pro Tyr Glu Cys Ile Asp Glu
 595 600 605
 Trp Thr Lys Asn Lys Thr His Val Asp Asn Ile Val Ile Leu Ser Asp
 610 615 620
 Met Met Ile Ala Glu Gly Tyr Ser Asp Ile Asn Val Arg Gly Ser Ser
 625 630 635 640
 Ile Val Asn Ser Ile Lys Lys Tyr Lys Asp Glu Val Asn Pro Asn Ile
 645 650 655
 Lys Ile Phe Ala Val Asp Leu Glu Gly Tyr Gly Lys Cys Leu Asn Leu
 660 665 670
 Gly Asp Glu Phe Asn Glu Asn Asn Tyr Ile Lys Ile Phe Gly Met Ser
 675 680 685
 Asp Ser Ile Leu Lys Phe Ile Ser Ala Lys Gln Gly Gly Ala Asn Met
 690 695 700
 Val Glu Val Ile Lys Asn Phe Ala Leu Gln Lys Ile Gly Gln Lys
 705 710 715

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2829 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 47..2665
- (D) OTHER INFORMATION: /codon= (seq: "taa", aa: Gln)
/seq: "tag", aa: Gln
/note= "Tetrahymena thermophila 95 kD
TRT protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TCAATACTAT	TAATTAATAA	ATAAAAAAAA	GCAAACTACA	AAGAAA	ATG	TCA	AGG	55
					Met	Ser	Arg	
							1	
CGT	AAC	TAA	AAA	AAG	CCA	TAG	GCT	103
Arg	Asn	Gln	Lys	Lys	Pro	Gln	Ala	
5	10	15						
GAT	TTT	GTA	TTA	CAA	AAT	CTA	GAA	151
Asp	Phe	Val	Leu	Gln	Asn	Leu	Glu	
20	25	30	35					
TAT	AAG	ACC	TAG	TAG	TAA	TAG	ATC	199
Tyr	Lys	Thr	Gln	Gln	Ile	Lys	Glu	
40	45	50						
AAG	TTC	AAA	AAT	TAA	GAT	TAG	GAT	247
Lys	Phe	Asn	Gln	Gln	Asp	Gln	Asp	
55	60	65						
GAT	GAA	GAA	AAC	AAC	TCA	AAT	AAA	295
Asp	Glu	Glu	Asn	Asn	Ser	Asn	Gly	
70	75	80						
AAT	TAG	ATT	AAG	TAG	CAA	GTT	TAA	343
Asn	Gln	Ile	Lys	Gln	Gln	Val	Gln	
85	90	95						
GTA	GAG	AAA	GAT	TTG	AAT	TTG	AAC	391
Val	Glu	Lys	Asp	Leu	Asn	Leu	Asn	
100	105	110						
CTT	TCT	GAA	TAG	CAA	GTG	AAA	GAA	439
Leu	Ser	Glu	Gln	Gln	Val	Lys	Glu	
120	125	130						
GAA	TAG	GTT	AAG	TAT	TAA	AAT	TTA	487
Glu	Gln	Val	Lys	Tyr	Gln	Asn	Leu	
135	140	145						

GAT TTA AAT GAG AGT GGT GGC CAT AGA AGA CAC AGA AGA GAA ACA GAT		535
Asp Leu Asn Glu Ser Gly Gly His Arg Arg His Arg Arg Glu Thr Asp		
150	155	160
TAT GAT ACT GAA AAA TGG TTT GAA ATA TCT CAT GAC CAA AAA AAT TAT		583
Tyr Asp Thr Glu Lys Trp Phe Glu Ile Ser His Asp Gln Lys Asn Tyr		
165	170	175
GTA TCA ATT TAC GCC AAC TAA AAG ACA TCA TAT TGT TGG TGG CTT AAA		631
Val Ser Ile Tyr Ala Asn Gln Lys Thr Ser Tyr Cys Trp Trp Leu Lys		
180	185	190
195		
GAT TAT TTT AAT AAA AAC AAT TAT GAT CAT CTT AAT GTA AGC ATT AAC		679
Asp Tyr Phe Asn Lys Asn Asn Tyr Asp His Leu Asn Val Ser Ile Asn		
200	205	210
AGA CTA GAA ACT GAA GCC GAA TTC TAT GCC TTT GAT GAT TTT TCA CAA		727
Arg Leu Glu Thr Glu Ala Glu Phe Tyr Ala Phe Asp Asp Phe Ser Gln		
215	220	225
ACA ATC AAA CTT ACT AAT TCT TAC TAG ACT GTT AAC ATA GAC GTT		775
Thr Ile Lys Leu Thr Asn Asn Ser Tyr Gln Thr Val Asn Ile Asp Val		
230	235	240
AAT TTT GAT AAT AAT CTC TGT ATA CTC GCA TTG CTT AGA TTT TTA TTA		823
Asn Phe Asp Asn Asn Leu Cys Ile Leu Ala Leu Leu Arg Phe Leu Leu		
245	250	255
TCA CTA GAA AGA TTC AAT ATT TTG AAT ATA AGA TCT TCT TAT ACA AGA		871
Ser Leu Glu Arg Phe Asn Ile Leu Asn Ile Arg Ser Ser Tyr Thr Arg		
260	265	270
275		
AAT TAA TAT AAT TTT GAG AAA ATT GGT GAG CTA CTT GAA ACT ATC TTC		919
Asn Gln Tyr Asn Phe Glu Lys Ile Gly Glu Leu Leu Glu Thr Ile Phe		
280	285	290
GCA GTT GTC TTT TCT CAT CGC CAC TTA CAA GGC ATT CAT TTA CAA GTT		967
Ala Val Val Phe Ser His Arg His Leu Gln Gly Ile His Leu Gln Val		
295	300	305
CCT TGC GAA GCG TTC TAA TAT TTA GTT AAC TCC TCA TCA TAA ATT AGC		1015
Pro Cys Glu Ala Phe Gln Tyr Leu Val Asn Ser Ser Gln Ile Ser		
310	315	320
GTT AAA GAT AGC TAA TTA TAG GTA TAC TCT TCT TCA GAC TTA AAA		1063
Val Lys Asp Ser Gln Leu Gln Val Tyr Ser Phe Ser Thr Asp Leu Lys		
325	330	335
TTA GTT GAC ACT AAC AAA GTC CAA GAT TAT TTT AAG TTC TTA TAA GAA		1111
Leu Val Asp Thr Asn Lys Val Gln Asp Tyr Phe Lys Phe Leu Gln Glu		
340	345	350
355		
TTC CCT CGT TTG ACT CAT GTA AGC TAG TAG GCT ATC CCA GTT AGT GCT		1159
Phe Pro Arg Leu Thr His Val Ser Gln Gln Ala Ile Pro Val Ser Ala		
360	365	370
ACT AAC GCT GTA GAG AAC CTC AAT GTT TTA CTT AAA AAG GTC AAG CAT		1207
Thr Asn Ala Val Glu Asn Leu Asn Val Leu Leu Lys Lys Val Lys His		
375	380	385

GCT AAT CTT AAT TTA GTT TCT ATC CCT ACC TAA TTC AAT TTT GAT TTC Ala Asn Leu Asn Leu Val Ser Ile Pro Thr Gln Phe Asn Phe Asp Phe 390 395 400	1255
TAC TTT GTT AAT TTA TAA CAT TTG AAA TTA GAG TTT GGA TTA GAA CCA Tyr Phe Val Asn Leu Gln His Leu Lys Leu Glu Phe Gly Leu Glu Pro 405 410 415	1303
AAT ATT TTG ACA AAA CAA AAG CTT GAA AAT CTA CTT TTG AGT ATA AAA Asn Ile Leu Thr Lys Gln Lys Leu Glu Asn Leu Leu Ser Ile Lys 420 425 430 435	1351
TAA TCA AAA AAT CTT AAA TTT TTA AGA TTA AAC TTT TAC ACC TAC GTT Gln Ser Lys Asn Leu Lys Phe Leu Arg Leu Asn Phe Tyr Thr Tyr Val 440 445 450	1399
GCT TAA GAA ACC TCC AGA AAA CAG ATA TTA AAA CAA GCT ACA ACA ATC Ala Gln Glu Thr Ser Arg Lys Gln Ile Leu Lys Gln Ala Thr Thr Ile 455 460 465	1447
AAA AAT CTC AAA AAC AAT AAA AAT CAA GAA GAA ACT CCT GAA ACT AAA Lys Asn Leu Lys Asn Asn Lys Asn Gln Glu Glu Thr Pro Glu Thr Lys 470 475 480	1495
GAT GAA ACT CCA AGC GAA AGC ACA AGT GGT ATG AAA TTT TTT GAT CAT Asp Glu Thr Pro Ser Glu Ser Thr Ser Gly Met Lys Phe Phe Asp His 485 490 495	1543
CTT TCT GAA TTA ACC GAG CTT GAA GAT TTC AGC GTT AAC TTG TAA GCT Leu Ser Glu Leu Thr Glu Leu Glu Asp Phe Ser Val Asn Leu Gln Ala 500 505 510 515	1591
ACC CAA GAA ATT TAT GAT AGC TTG CAC AAA CTT TTG ATT AGA TCA ACA Thr Gln Glu Ile Tyr Asp Ser Leu His Lys Leu Leu Ile Arg Ser Thr 520 525 530	1639
AAT TTA AAG AAG TTC AAA TTA AGT TAC AAA TAT GAA ATG GAA AAG AGT Asn Leu Lys Lys Phe Lys Leu Ser Tyr Lys Tyr Glu Met Glu Lys Ser 535 540 545	1687
AAA ATG GAT ACA TTC ATA GAT CTT AAG AAT ATT TAT GAA ACC TTA AAC Lys Met Asp Thr Phe Ile Asp Leu Lys Asn Ile Tyr Glu Thr Leu Asn 550 555 560	1735
AAT CTT AAA AGA TGC TCT GTT AAT ATA TCA AAT CCT CAT GGA AAC ATT Asn Leu Lys Arg Cys Ser Val Asn Ile Ser Asn Pro His Gly Asn Ile 565 570 575	1783
TCT TAT GAA CTG ACA AAT AAA GAT TCT ACT TTT TAT AAA TTT AAG CTG Ser Tyr Glu Leu Thr Asn Lys Asp Ser Thr Phe Tyr Lys Phe Lys Leu 580 585 590 595	1831
ACC TTA AAC TAA GAA TTA TAA CAC GCT AAG TAT ACT TTT AAG TAG AAC Thr Leu Asn Gln Glu Leu Gln His Ala Lys Tyr Thr Phe Lys Gln Asn 600 605 610	1879
GAA TTT TAA TTT AAT AAC GTT AAA AGT GCA AAA ATT GAA TCT TCC TCA Glu Phe Gln Phe Asn Asn Val Lys Ser Ala Lys Ile Glu Ser Ser Ser 615 620 625	1927

TTA GAA AGC TTA GAA GAT ATT GAT AGT CTT TGC AAA TCT ATT GCT TCT Leu Glu Ser Leu Glu Asp Ile Asp Ser Leu Cys Lys Ser Ile Ala Ser 630 635 640	1975
TGT AAA AAT TTA CAA AAT GTT AAT ATT ATC GCC AGT TTG CTC TAT CCC Cys Lys Asn Leu Gln Asn Val Asn Ile Ile Ala Ser Leu Leu Tyr Pro 645 650 655	2023
AAC AAT ATT TAG AAA AAT CCT TTC AAT AAG CCC AAT CTT CTA TTT TTC Asn Asn Ile Gln Lys Asn Pro Phe Asn Lys Pro Asn Leu Leu Phe Phe 660 665 670 675	2071
AAG CAA TTT GAA TAA TTG AAA AAT TTG GAA AAT GTA TCT ATC AAC TGT Lys Gln Phe Glu Gln Leu Lys Asn Leu Glu Asn Val Ser Ile Asn Cys 680 685 690	2119
ATT CTT GAT CAG CAT ATA CTT AAT TCT ATT TCA GAA TTC TTA GAA AAG Ile Leu Asp Gln His Ile Leu Asn Ser Ile Ser Glu Phe Leu Glu Lys 695 700 705	2167
AAT AAA AAA ATA AAA GCA TTC ATT TTG AAA AGA TAT TAT TTA TTA CAA Asn Lys Ile Lys Ala Phe Ile Leu Lys Arg Tyr Tyr Leu Leu Gln 710 715 720	2215
TAT TAT CTT GAT TAT ACT AAA TTA TTT AAA ACA CTT CAA TAG TTA CCT Tyr Tyr Leu Asp Tyr Thr Lys Leu Phe Lys Thr Leu Gln Gln Leu Pro 725 730 735	2263
GAA TTA AAT TAA GTT TAC ATT AAT TAG CAA TTA GAA GAA TTG ACT GTG Glu Leu Asn Gln Val Tyr Ile Asn Gln Gln Leu Glu Glu Leu Thr Val 740 745 750 755	2311
AGT GAA GTA CAT AAG TAA GTA TGG GAA AAC CAC AAG CAA AAA GCT TTC Ser Glu Val His Lys Gln Val Trp Glu Asn His Lys Gln Lys Ala Phe 760 765 770	2359
TAT GAA CCA TTA TGT GAG TTT ATC AAA GAA TCA TCC TAA ACC CTT TAG Tyr Glu Pro Leu Cys Glu Phe Ile Lys Glu Ser Ser Gln Thr Leu Gln 775 780 785	2407
CTA ATA GAT TTT GAC CAA AAC ACT GTA AGT GAT GAC TCT ATT AAA AAG Leu Ile Asp Phe Asp Gln Asn Thr Val Ser Asp Asp Ser Ile Lys Lys 790 795 800	2455
ATT TTA GAA TCT ATA TCT GAG TCT AAG TAT CAT CAT TAT TTG AGA TTG Ile Leu Glu Ser Ile Ser Glu Ser Lys Tyr His His Tyr Leu Arg Leu 805 810 815	2503
AAC CCT AGT TAA TCT AGC AGT TTA ATT AAA TCT GAA AAC GAA GAA ATT Asn Pro Ser Gln Ser Ser Leu Ile Lys Ser Glu Asn Glu Glu Ile 820 825 830 835	2551
TAA GAA CTT CTC AAA GCT TGC GAC GAA AAA GGT GTT TTA GTA AAA GCA Gln Glu Leu Leu Lys Ala Cys Asp Glu Lys Gly Val Leu Val Lys Ala 840 845 850	2599
TAC TAT AAA TTC CCT CTA TGT TTA CCA ACT GGT ACT TAT TAC GAT TAC Tyr Tyr Lys Phe Pro Leu Cys Leu Pro Thr Gly Thr Tyr Tyr Asp Tyr 855 860 865	2647

AAT TCA GAT AGA TGG TGATTAATTA AATATTAGTT TAAATAAATA TTAAATATTG	2702
Asn Ser Asp Arg Trp	
870	
AATATTTCTT TGCTTATTAT TTGAATAATA CATAACAATAG TCATTTTAG TGTTTGAAT	2762
ATATTTAGT TATTAATTC ATTATTTAA GTAAATAATT ATTTTCAT CATTTTTAA	2822
AAAATCG	2829

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 872 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met Ser Arg Arg Asn Gln Lys Lys Pro Gln Ala Pro Ile Gly Asn Glu			
1	5	10	15
Thr Asn Leu Asp Phe Val Leu Gln Asn Leu Glu Val Tyr Lys Ser Gln			
20	25	30	
Ile Glu His Tyr Lys Thr Gln Gln Gln Ile Lys Glu Glu Asp Leu			
35	40	45	
Lys Leu Leu Lys Phe Lys Asn Gln Asp Gln Asp Gly Asn Ser Gly Asn			
50	55	60	
Asp Asp Asp Asp Glu Glu Asn Asn Ser Asn Lys Gln Gln Glu Leu Leu			
65	70	75	80
Arg Arg Val Asn Gln Ile Lys Gln Gln Val Gln Leu Ile Lys Lys Val			
85	90	95	
Gly Ser Lys Val Glu Lys Asp Leu Asn Leu Asn Glu Asp Glu Asn Lys			
100	105	110	
Lys Asn Gly Leu Ser Glu Gln Val Lys Glu Glu Gln Leu Arg Thr			
115	120	125	
Ile Thr Glu Glu Gln Val Lys Tyr Gln Asn Leu Val Phe Asn Met Asp			
130	135	140	
Tyr Gln Leu Asp Leu Asn Glu Ser Gly Gly His Arg Arg His Arg Arg			
145	150	155	160
Glu Thr Asp Tyr Asp Thr Glu Lys Trp Phe Glu Ile Ser His Asp Gln			
165	170	175	
Lys Asn Tyr Val Ser Ile Tyr Ala Asn Gln Lys Thr Ser Tyr Cys Trp			
180	185	190	
Trp Leu Lys Asp Tyr Phe Asn Lys Asn Asn Tyr Asp His Leu Asn Val			
195	200	205	

Ser Ile Asn Arg Leu Glu Thr Glu Ala Glu Phe Tyr Ala Phe Asp Asp
 210 215 220

Phe Ser Gln Thr Ile Lys Leu Thr Asn Asn Ser Tyr Gln Thr Val Asn
 225 230 235 240

Ile Asp Val Asn Phe Asp Asn Asn Leu Cys Ile Leu Ala Leu Leu Arg
 245 250 255

Phe Leu Leu Ser Leu Glu Arg Phe Asn Ile Leu Asn Ile Arg Ser Ser
 260 265 270

Tyr Thr Arg Asn Gln Tyr Asn Phe Glu Lys Ile Gly Glu Leu Leu Glu
 275 280 285

Thr Ile Phe Ala Val Val Phe Ser His Arg His Leu Gln Gly Ile His
 290 295 300

Leu Gln Val Pro Cys Glu Ala Phe Gln Tyr Leu Val Asn Ser Ser Ser
 305 310 315 320

Gln Ile Ser Val Lys Asp Ser Gln Leu Gln Val Tyr Ser Phe Ser Thr
 325 330 335

Asp Leu Lys Leu Val Asp Thr Asn Lys Val Gln Asp Tyr Phe Lys Phe
 340 345 350

Leu Gln Glu Phe Pro Arg Leu Thr His Val Ser Gln Gln Ala Ile Pro
 355 360 365

Val Ser Ala Thr Asn Ala Val Glu Asn Leu Asn Val Leu Leu Lys Lys
 370 375 380

Val Lys His Ala Asn Leu Asn Leu Val Ser Ile Pro Thr Gln Phe Asn
 385 390 395 400

Phe Asp Phe Tyr Phe Val Asn Leu Gln His Leu Lys Leu Glu Phe Gly
 405 410 415

Leu Glu Pro Asn Ile Leu Thr Lys Gln Lys Leu Glu Asn Leu Leu Leu
 420 425 430

Ser Ile Lys Gln Ser Lys Asn Leu Lys Phe Leu Arg Leu Asn Phe Tyr
 435 440 445

Thr Tyr Val Ala Gln Glu Thr Ser Arg Lys Gln Ile Leu Lys Gln Ala
 450 455 460

Thr Thr Ile Lys Asn Leu Lys Asn Asn Lys Asn Gln Glu Glu Thr Pro
 465 470 475 480

Glu Thr Lys Asp Glu Thr Pro Ser Glu Ser Thr Ser Gly Met Lys Phe
 485 490 495

Phe Asp His Leu Ser Glu Leu Thr Glu Leu Glu Asp Phe Ser Val Asn
 500 505 510

Leu Gln Ala Thr Gln Glu Ile Tyr Asp Ser Leu His Lys Leu Leu Ile
 515 520 525

Arg Ser Thr Asn Leu Lys Lys Phe Lys Leu Ser Tyr Lys Tyr Glu Met
 530 535 540
 Glu Lys Ser Lys Met Asp Thr Phe Ile Asp Leu Lys Asn Ile Tyr Glu
 545 550 555 560
 Thr Leu Asn Asn Leu Lys Arg Cys Ser Val Asn Ile Ser Asn Pro His
 565 570 575
 Gly Asn Ile Ser Tyr Glu Leu Thr Asn Lys Asp Ser Thr Phe Tyr Lys
 580 585 590
 Phe Lys Leu Thr Leu Asn Gln Glu Leu Gln His Ala Lys Tyr Thr Phe
 595 600 605
 Lys Gln Asn Glu Phe Gln Phe Asn Asn Val Lys Ser Ala Lys Ile Glu
 610 615 620
 Ser Ser Ser Leu Glu Ser Leu Glu Asp Ile Asp Ser Leu Cys Lys Ser
 625 630 635 640
 Ile Ala Ser Cys Lys Asn Leu Gln Asn Val Asn Ile Ile Ala Ser Leu
 645 650 655
 Leu Tyr Pro Asn Asn Ile Gln Lys Asn Pro Phe Asn Lys Pro Asn Leu
 660 665 670
 Leu Phe Phe Lys Gln Phe Glu Gln Leu Lys Asn Leu Glu Asn Val Ser
 675 680 685
 Ile Asn Cys Ile Leu Asp Gln His Ile Leu Asn Ser Ile Ser Glu Phe
 690 695 700
 Leu Glu Lys Asn Lys Lys Ile Lys Ala Phe Ile Leu Lys Arg Tyr Tyr
 705 710 715 720
 Leu Leu Gln Tyr Tyr Leu Asp Tyr Thr Lys Leu Phe Lys Thr Leu Gln
 725 730 735
 Gln Leu Pro Glu Leu Asn Gln Val Tyr Ile Asn Gln Gln Leu Glu Glu
 740 745 750
 Leu Thr Val Ser Glu Val His Lys Gln Val Trp Glu Asn His Lys Gln
 755 760 765
 Lys Ala Phe Tyr Glu Pro Leu Cys Glu Phe Ile Lys Glu Ser Ser Gln
 770 775 780
 Thr Leu Gln Leu Ile Asp Phe Asp Gln Asn Thr Val Ser Asp Asp Ser
 785 790 795 800
 Ile Lys Lys Ile Leu Glu Ser Ile Ser Glu Ser Lys Tyr His His Tyr
 805 810 815
 Leu Arg Leu Asn Pro Ser Gln Ser Ser Ser Leu Ile Lys Ser Glu Asn
 820 825 830
 Glu Glu Ile Gln Glu Leu Leu Lys Ala Cys Asp Glu Lys Gly Val Leu
 835 840 845

Val	Lys	Ala	Tyr	Tyr	Lys	Phe	Pro	Leu	Cys	Leu	Pro	Thr	Gly	Thr	Tyr
850					855						860				
Tyr	Asp	Tyr	Asn	Ser	Asp	Arg	Trp								
865				870											

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 884 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..884
- (D) OTHER INFORMATION: /note= "Saccharomyces cerevisiae
L8543.12 (Est2p) protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Met	Lys	Ile	Leu	Phe	Glu	Phe	Ile	Gln	Asp	Lys	Leu	Asp	Ile	Asp	Leu
1				5				10					15		
Gln	Thr	Asn	Ser	Thr	Tyr	Lys	Glu	Asn	Leu	Lys	Cys	Gly	His	Phe	Asn
				20				25					30		
Gly	Leu	Asp	Glu	Ile	Leu	Thr	Thr	Cys	Phe	Ala	Leu	Pro	Asn	Ser	Arg
				35				40				45			
Lys	Ile	Ala	Leu	Pro	Cys	Leu	Pro	Gly	Asp	Leu	Ser	His	Lys	Ala	Val
				50				55			60				
Ile	Asp	His	Cys	Ile	Ile	Tyr	Leu	Leu	Thr	Gly	Glu	Leu	Tyr	Asn	Asn
				65			70			75			80		
Val	Leu	Thr	Phe	Gly	Tyr	Lys	Ile	Ala	Arg	Asn	Glu	Asp	Val	Asn	Asn
				85				90					95		
Ser	Leu	Phe	Cys	His	Ser	Ala	Asn	Val	Asn	Val	Thr	Leu	Leu	Lys	Gly
				100				105				110			
Ala	Ala	Trp	Lys	Met	Phe	His	Ser	Leu	Val	Gly	Thr	Tyr	Ala	Phe	Val
				115				120			125				
Asp	Leu	Leu	Ile	Asn	Tyr	Thr	Val	Ile	Gln	Phe	Asn	Gly	Gln	Phe	Phe
				130			135			140					
Thr	Gln	Ile	Val	Gly	Asn	Arg	Cys	Asn	Glu	Pro	His	Leu	Pro	Pro	Lys
				145			150			155			160		
Trp	Val	Gln	Arg	Ser	Ser	Ser	Ser	Ser	Ala	Thr	Ala	Ala	Gln	Ile	Lys
				165				170				175			

Gln Leu Thr Glu Pro Val Thr Asn Lys Gln Phe Leu His Lys Leu Asn
 180 185 190
 Ile Asn Ser Ser Ser Phe Phe Pro Tyr Ser Lys Ile Leu Pro Ser Ser
 195 200 205
 Ser Ser Ile Lys Lys Leu Thr Asp Leu Arg Glu Ala Ile Phe Pro Thr
 210 215 220
 Asn Leu Val Lys Ile Pro Gln Arg Leu Lys Val Arg Ile Asn Leu Thr
 225 230 235 240
 Leu Gln Lys Leu Leu Lys Arg His Lys Arg Leu Asn Tyr Val Ser Ile
 245 250 255
 Leu Asn Ser Ile Cys Pro Pro Leu Glu Gly Thr Val Leu Asp Leu Ser
 260 265 270
 His Leu Ser Arg Gln Ser Pro Lys Glu Arg Val Leu Lys Phe Ile Ile
 275 280 285
 Val Ile Leu Gln Lys Leu Leu Pro Gln Glu Met Phe Gly Ser Lys Lys
 290 295 300
 Asn Lys Gly Lys Ile Ile Lys Asn Leu Asn Leu Leu Leu Ser Leu Pro
 305 310 315 320
 Leu Asn Gly Tyr Leu Pro Phe Asp Ser Leu Leu Lys Lys Leu Arg Leu
 325 330 335
 Lys Asp Phe Arg Trp Leu Phe Ile Ser Asp Ile Trp Phe Thr Lys His
 340 345 350
 Asn Phe Glu Asn Leu Asn Gln Leu Ala Ile Cys Phe Ile Ser Trp Leu
 355 360 365
 Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr Cys Thr
 370 375 380
 Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp Thr Trp
 385 390 395 400
 Asn Lys Leu Ile Thr Pro Phe Ile Val Glu Tyr Phe Lys Thr Tyr Leu
 405 410 415
 Val Glu Asn Asn Val Cys Arg Asn His Asn Ser Tyr Thr Leu Ser Asn
 420 425 430
 Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn Asn Glu
 435 440 445
 Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp Glu Glu Glu Phe
 450 455 460
 Thr Ile Tyr Lys Glu Asn His Lys Asn Ala Ile Gln Pro Thr Gln Lys
 465 470 475 480
 Ile Leu Glu Tyr Leu Arg Asn Lys Arg Pro Thr Ser Phe Thr Lys Ile
 485 490 495

Tyr Ser Pro Thr Gln Ile Ala Asp Arg Ile Lys Glu Phe Lys Gln Arg
 500 505 510

Leu Leu Lys Lys Phe Asn Asn Val Leu Pro Glu Leu Tyr Phe Met Lys
 515 520 525

Phe Asp Val Lys Ser Cys Tyr Asp Ser Ile Pro Arg Met Glu Cys Met
 530 535 540

Arg Ile Leu Lys Asp Ala Leu Lys Asn Glu Asn Gly Phe Phe Val Arg
 545 550 555 560

Ser Gln Tyr Phe Phe Asn Thr Asn Thr Gly Val Leu Lys Leu Phe Asn
 565 570 575

Val Val Asn Ala Ser Arg Val Pro Lys Pro Tyr Glu Leu Tyr Ile Asp
 580 585 590

Asn Val Arg Thr Val His Leu Ser Asn Gln Asp Val Ile Asn Val Val
 595 600 605

Glu Met Glu Ile Phe Lys Thr Ala Leu Trp Val Glu Asp Lys Cys Tyr
 610 615 620

Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro Ile
 625 630 635 640

Val Asp Leu Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser Glu Phe Lys
 645 650 655

Ala Ser Pro Ser Gln Asp Thr Leu Ile Leu Lys Leu Ala Asp Asp Phe
 660 665 670

Leu Ile Ile Ser Thr Asp Gln Gln Gln Val Ile Asn Ile Lys Lys Leu
 675 680 685

Ala Met Gly Gly Phe Gln Lys Tyr Asn Ala Lys Ala Asn Arg Asp Lys
 690 695 700

Ile Leu Ala Val Ser Ser Gln Ser Asp Asp Asp Thr Val Ile Gln Phe
 705 710 715 720

Cys Ala Met His Ile Phe Val Lys Glu Leu Glu Val Trp Lys His Ser
 725 730 735

Ser Thr Met Asn Asn Phe His Ile Arg Ser Lys Ser Ser Lys Gly Ile
 740 745 750

Phe Arg Ser Leu Ile Ala Leu Phe Asn Thr Arg Ile Ser Tyr Lys Thr
 755 760 765

Ile Asp Thr Asn Leu Asn Ser Thr Asn Thr Val Leu Met Gln Ile Asp
 770 775 780

His Val Val Lys Asn Ile Ser Glu Cys Tyr Lys Ser Ala Phe Lys Asp
 785 790 795 800

Leu Ser Ile Asn Val Thr Gln Asn Met Gln Phe His Ser Phe Leu Gln
 805 810 815

Arg Ile Ile Glu Met Thr Val Ser Gly Cys Pro Ile Thr Lys Cys Asp
820 825 830

Pro Leu Ile Glu Tyr Glu Val Arg Phe Thr Ile Leu Asn Gly Phe Leu
835 840 845

Glu Ser Leu Ser Ser Asn Thr Ser Lys Phe Lys Asp Asn Ile Ile Leu
850 855 860

Leu Arg Lys Glu Ile Gln His Leu Gln Ala Tyr Ile Tyr Ile Tyr Ile
865 870 875 880

His Ile Val Asn

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

YARACHAARG GHATYCCHYA RGG

23

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

DGTDATNARN ARRTARTCRT C

21

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Leu Cys Val Ser Tyr Ile Leu Ser Ser Phe Tyr Tyr Ala Asn Leu Glu
1 5 10 15
Glu Asn Ala Leu Gln Phe Leu Arg Lys Glu Ser Met Asp Pro Glu Lys
20 25 30
Pro Glu Thr Asn Leu Leu Met Arg Leu Thr
35 40

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Leu Cys Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu
1 5 10 15
Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro Glu Asn
20 25 30
Pro Asn Val Asn Leu Leu Met Arg Leu Thr
35 40

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /mod_base= OTHER
/note= "N = thymidine modified by a biotin group"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 12..13
- (D) OTHER INFORMATION: /mod_base= gm

(ix) FEATURE:
(A) NAME/KEY: modified_base
(B) LOCATION: 14..17
(D) OTHER INFORMATION: /mod_base= um

(ix) FEATURE:
(A) NAME/KEY: modified_base
(B) LOCATION: 18..21
(D) OTHER INFORMATION: /mod_base= gm

(ix) FEATURE:
(A) NAME/KEY: modified_base
(B) LOCATION: 22..25
(D) OTHER INFORMATION: /mod_base= um

(ix) FEATURE:
(A) NAME/KEY: modified_base
(B) LOCATION: 26
(D) OTHER INFORMATION: /mod_base= gm

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

NAGACCTGTT ANNNNNNNNN NNNNNN

26

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GGGGTTTTGG GGTTTT

16

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 389 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..389
(D) OTHER INFORMATION: /note= "partial sequence of a cDNA
encoding human telomerase peptide
motifs (EST AA281296)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GCCAAGTTCC	TGCACGGCT	GATGAGTGTG	TACGTCGTCG	AGCTGCTCAG	GTCTTCCTT	60
TATGTCACGG	AGACCACGTT	TCAAAAGAAC	AGGCTTTTT	TCTACCGGAA	GAGTGTCTGG	120
AGCAAGTTGC	AAAGCATTGG	AATCAGACAG	CACTTGAAGA	GGGTGCAGCT	GCAGGACGTG	180
TCGGAAGCAG	AGGTCAGGCA	GCATCGGGAA	GCCAGGCCCG	CCCTGCTGAC	GTCCAGACTC	240
CGCTTCATCC	CCAAGCCTGA	CGGGCTGCGG	CCGATTGTGA	ACATGGACTA	CGTCGTGGGA	300
GCCAGAACGT	TCCGCAGAGA	AAAGAGGGCC	GAGCGTCTCA	CCTCGAGGGT	GAAGGCAC TG	360
TTCAGCGTGC	TCAACTACGA	GCAGGGCGCG				389

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Ile	Ser	Glu	Ile	Glu	Trp	Leu	Val	Leu	Gly	Lys	Arg	Ser	Asn	Ala	Lys
1					5				10						15
Met	Cys	Leu	Ser	Asp	Phe	Glu	Lys	Arg	Lys	Gln	Ile	Phe	Ala	Glu	Phe
					20				25						30
Ile	Tyr	Trp	Leu	Tyr	Asn	Ser	Phe	Ile	Ile	Pro	Ile	Leu	Gln	Ser	Phe
					35			40							45
Phe	Tyr	Ile	Thr	Glu	Ser	Ser	Asp	Leu	Arg	Asn	Arg	Thr	Val	Tyr	Phe
					50			55							60
Arg	Lys	Asp	Ile	Trp	Lys	Leu	Leu	Cys	Arg	Pro	Phe	Ile	Thr	Ser	Met
					65			70			75				80
Lys	Met	Glu	Ala	Phe	Glu	Lys	Ile	Asn	Glu	Asn	Asn	Val	Arg	Met	Asp
					85				90						95
Thr	Gln	Lys	Thr	Thr	Leu	Pro	Pro	Ala	Val	Ile	Arg	Leu	Leu	Pro	Lys
					100				105						110
Lys	Asn	Thr	Phe	Arg	Leu	Ile	Thr	Asn	Leu	Arg	Lys	Arg	Phe	Leu	Ile
					115				120						125
Lys	Met	Gly	Ser	Asn	Lys	Lys	Met	Leu	Val	Ser	Thr	Asn	Gln	Thr	Leu
					130			135							140
Arg	Pro	Val	Ala	Ser	Ile	Leu	Lys	His	Leu	Ile	Asn	Glu	Glu	Ser	Ser
					145			150			155				160

Gly Ile Pro Phe Asn Leu Glu Val Tyr Met Lys Leu Leu Thr Phe Lys
 165 170 175
 Lys Asp Leu Leu Lys His Arg Met Phe Gly Arg Lys Lys Tyr Phe Val
 180 185 190
 Arg Ile Asp Ile Lys Ser Cys Tyr Asp Arg Ile Lys Gln Asp Leu Met
 195 200 205
 Phe Arg Ile Val Lys Lys Leu Lys Asp Pro Glu Phe Val Ile Arg
 210 215 220
 Lys Tyr Ala Thr Ile His Ala Thr Ser
 225 230

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 233 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Leu Lys Asp Phe Arg Trp Leu Phe Ile Ser Asp Ile Trp Phe Thr Lys
 1 5 10 15
 His Asn Phe Glu Asn Leu Asn Gln Leu Ala Ile Cys Phe Ile Ser Trp
 20 25 30
 Leu Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr Cys
 35 40 45
 Thr Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp Thr
 50 55 60
 Trp Asn Lys Leu Ile Thr Pro Phe Ile Val Glu Tyr Phe Lys Thr Tyr
 65 70 75 80
 Leu Val Glu Asn Asn Val Cys Arg Asn His Asn Ser Tyr Thr Leu Ser
 85 90 95
 Asn Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn Asn
 100 105 110
 Glu Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp Glu Glu Glu
 115 120 125
 Phe Thr Ile Tyr Lys Glu Asn His Lys Asn Ala Ile Gln Pro Thr Gln
 130 135 140
 Lys Ile Leu Glu Tyr Leu Arg Asn Lys Arg Pro Thr Ser Phe Thr Lys
 145 150 155 160
 Ile Tyr Ser Pro Thr Gln Ile Ala Asp Arg Ile Lys Glu Phe Lys Gln
 165 170 175

Arg Leu Leu Lys Lys Phe Asn Asn Val Leu Pro Glu Leu Tyr Phe Met
 180 185 190
 Lys Phe Asp Val Lys Ser Cys Tyr Asp Ser Ile Pro Arg Met Glu Cys
 195 200 205
 Met Arg Ile Leu Lys Asp Ala Leu Lys Asn Glu Asn Gly Phe Phe Val
 210 215 220
 Arg Ser Gln Tyr Phe Phe Asn Thr Asn
 225 230

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 233 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Thr Arg Glu Ile Ser Trp Met Gln Val Glu Thr Ser Ala Lys His Phe
 1 5 10 15
 Tyr Tyr Phe Asp His Glu Asn Ile Tyr Val Leu Trp Lys Leu Leu Arg
 20 25 30
 Trp Ile Phe Glu Asp Leu Val Val Ser Leu Ile Arg Cys Phe Phe Tyr
 35 40 45
 Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys
 50 55 60
 Asn Ile Trp Asp Val Ile Met Lys Met Ser Ile Ala Asp Leu Lys Lys
 65 70 75 80
 Glu Thr Leu Ala Glu Val Gln Glu Lys Glu Val Glu Glu Trp Lys Lys
 85 90 95
 Ser Leu Gly Phe Ala Pro Gly Lys Leu Arg Leu Ile Pro Lys Lys Thr
 100 105 110
 Thr Phe Arg Pro Ile Met Thr Phe Asn Lys Lys Ile Val Asn Ser Asp
 115 120 125
 Arg Lys Thr Thr Lys Leu Thr Thr Asn Thr Lys Leu Leu Asn Ser His
 130 135 140
 Leu Met Leu Lys Thr Leu Lys Asn Arg Met Phe Lys Asp Pro Phe Gly
 145 150 155 160
 Phe Ala Val Phe Asn Tyr Asp Asp Val Met Lys Lys Tyr Glu Glu Phe
 165 170 175
 Val Cys Lys Trp Lys Gln Val Gly Gln Pro Lys Leu Phe Phe Ala Thr
 180 185 190

Met	Asp	Ile	Glu	Lys	Cys	Tyr	Asp	Ser	Val	Asn	Arg	Glu	Lys	Leu	Ser
195														200	205
Thr	Phe	Leu	Lys	Thr	Thr	Lys	Leu	Leu	Ser	Ser	Asp	Phe	Trp	Ile	Met
210							215							220	
Thr	Ala	Gln	Ile	Leu	Lys	Arg	Lys	Asn							
225					230										

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2631
- (D) OTHER INFORMATION: /note= "Saccharomyces cerevisiae Est 2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ATTTATACTC	ATGAAAATCT	TATTCGAGTT	CATTCAAGAC	AAGCTTGACA	TTGATCTACA	60
GACCAACAGT	ACTTACAAAG	AAAATTTAAA	ATGTGGTCAC	TTCAATGGCC	TCGATGAAAT	120
TCTAACTACG	TGTTTCGCAC	TACCAAATTC	AAGAAAAATA	GCATTACCAT	GCCTTCCTGG	180
TGACTTAAGC	CACAAAGCAG	TCATTGATCA	CTGCATCATT	TACCTGTTGA	CGGGCGAATT	240
ATACAACAAAC	GTACTAACAT	TTGGCTATAA	AATAGCTAGA	AATGAAGATG	TCAACAATAG	300
TCTTTTTTGC	CATTCTGCAA	ATGTTAACGT	TACGTTACTG	AAAGGCGCTG	CTTGGAAAAT	360
GTTCCACAGT	TTGGTCGGTA	CATACGCATT	CGTTGATTAA	TTGATCAATT	ATACAGTAAT	420
TCAATTAAAT	GGGCAGTTTT	TCACTCAAAT	CGTGGGTAAC	AGATGTAACG	AACCTCATCT	480
GCCGCCAAA	TGGGTCCAAC	GATCATCCCTC	ATCATCCGCA	ACTGCTGCGC	AAATCAAACA	540
ACTTACAGAA	CCAGTGACAA	ATAAACAAATT	CTTACACAAG	CTCAATATAA	ATTCCTCTTC	600
TTTTTTTCCT	TATAGCAAGA	TCCTTCCTTC	ATCATCATCT	ATCAAAAAGC	TAACTGACTT	660
GAGAGAAGCT	ATTTTTCCCA	CAAATTTGGT	TAAAATTCT	CAGAGACTAA	AGGTACGAAT	720
TAATTTGACG	CTGCCAAGAC	TATTAAGAG	ACATAAGCGT	TTGAATTACG	TTTCTATTTT	780
GAATAGTATT	TGCCACCACAT	TGGAAGGGAC	CGTATTGGAC	TTGTCGCATT	TGAGTAGGCA	840
ATCACCAAAG	GAACGAGTCT	TGAAATTAT	CATTGTTATT	TTACAGAAGT	TATTACCCCA	900
AGAAATGTTT	GGCTCAAAGA	AAAATAAAGG	AAAATTATC	AAGAATCTAA	ATCTTTTATT	960

AAGTTTACCC	TTAAATGGCT	ATTTACCATT	TGATAGTTG	TTGAAAAAGT	TAAGATTAAA	1020
GGATTTTCGG	TGGTTGTTCA	TTCTGATAT	TTGGTCACC	AAGCACAATT	TTGAAAACCTT	1080
GAATCAATTG	GCGATTGTT	TCATTCCTG	GCTATTTAGA	CAACTAATTC	CCAAAATTAT	1140
ACAGACTTTT	TTTTACTGCA	CCGAAATATC	TTCTACAGTG	ACAATTGTTT	ACTTTAGACA	1200
TGATACTTGG	AATAAACTTA	TCACCCCTT	TATCGTAGAA	TATTTAAGA	CGTACTTAGT	1260
CGAAAACAAAC	GTATGTAGAA	ACCATAATAG	TTACACGTTG	TCCAATTCA	ATCATAGCAA	1320
AATGAGGATT	ATACCAAAAAA	AAAGTAATAA	TGAGTTCAGG	ATTATTGCCA	TCCCATGCAG	1380
AGGGGCAGAC	GAAGAAGAAT	TCACAATTAA	TAAGGAGAAT	CACAAAAATG	CTATCCAGCC	1440
CACTCAAAAAA	ATTTAGAAT	ACCTAAGAAA	CAAAAGGCCG	ACTAGTTTA	CTAAAATATA	1500
TTCTCCAACG	CAAATAGCTG	ACCGTATCAA	AGAATTAAAG	CAGAGACTTT	TAAAGAAATT	1560
TAATAATGTC	TTACCAGAGC	TTTATTCAT	GAAATTGAT	GTCAAATCTT	GCTATGATT	1620
CATACCAAGG	ATGGAATGTA	TGAGGATACT	CAAGGATGCG	CTAAAAAATG	AAAATGGTT	1680
TTTCGTTAGA	TCTCAATATT	TCTTCATAC	CAATACAGGT	GTATTGAAGT	TATTTAATGT	1740
TGTTAACGCT	AGCAGAGTAC	CAAAACCTTA	TGAGCTATAC	ATAGATAATG	TGAGGACGGT	1800
TCATTTATCA	AATCAGGATG	TTATAAACGT	TGTAGAGATG	GAAATATTAA	AAACAGCTTT	1860
GTGGGTTGAA	GATAAGTGCT	ACATTAGAGA	AGATGGTCTT	TTTCAGGGCT	CTAGTTTATC	1920
TGCTCCGATC	GTTGATTGG	TGTATGACGA	TCTTCTGGAG	TTTTATAGCG	AGTTTAAAGC	1980
CAGTCCTAGC	CAGGACACAT	TAATTTAAA	ACTGGCTGAC	GATTTCTTA	TAATATCAAC	2040
AGACCAACAG	CAAGTGATCA	ATATCAAAAAA	GCTTGCCATG	GGCGGATTT	AAAAATATAA	2100
TGCGAAAGCC	AATAGAGACA	AAATTTAGC	CGTAAGCTCC	CAATCAGATG	ATGATACGGT	2160
TATTCAATT	TGTGCAATGC	ACATATTGT	TAAAGAATTG	GAAGTTGGA	AACATTCAAG	2220
CACAATGAAT	AATTCATA	TCCGTTCGAA	ATCTAGTAAA	GGGATATTTC	GAAGTTAAT	2280
AGCGCTGTT	AACACTAGAA	TCTCTTATAA	AACAATTGAC	ACAAATTAA	ATTCAACAAA	2340
CACCGTTCTC	ATGCAAATTG	ATCATGTTGT	AAAGAACATT	TCGGAATGTT	ATAAATCTGC	2400
TTTTAAGGAT	CTATCAATT	ATGTTACGCA	AAATATGCAA	TTTCATTGCGT	TCTTACAACG	2460
CATCATTGAA	ATGACAGTCA	GCGGTTGTCC	AATTACGAAA	TGTGATCCTT	TAATCGAGTA	2520
TGAGGTACGA	TTCAACCATA	TGAATGGATT	TTGGAAAGC	CTATCTCAA	ACACATCAA	2580
ATTTAAAGAT	AATATCATTC	TTTGAGAAA	GGAAATTCAA	CACTTGCAAG	C	2631

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu
1 5 10 15

Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu
20 25 30

Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile
35 40 45

Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu
50 55 60

Val Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu
65 70 75 80

Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp
85 90 95

Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg
100 105 110

Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg
115 120 125

Ala

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(959..1216, 1273..1353, 1425..1543, 1595
..1857, 1894..2286, 2326..2396, 2436..2705, 2746
..2862, 2914..3083, 3125..3309, 3356..3504, 3546
..3759, 3797..4046, 4086..4252, 4296..4392, 4435
..4594)
- (D) OTHER INFORMATION: /note= "Saccharomyces pombe telomerase
catalytic subunit (TRT)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GGTACCGATT TACTTCCTT TCTTCATAAG CTAATTGCTT CCTCGAACGC TCCTAAATCT	60
CTGGAAATAT TTTTACAAGA ACTCAATAAC AATACCAAGT CAAATTCCAA TATGAAGGTG	120
TTATTAGTGA TCGATAATAT TTCTATTTA TCGGTCGTTA CCAAGTATAA GGACAAAAAG	180
AACAACTTCC TTCCCCCTAA AGACTTTAC TTTATTAATT TACTTTCAA ATATATTTCG	240
GGTTCGCTTA CTTTAATCG TGGTACTGTT TTAGCTGCTA CTTCTAGCCA ACCGCGTGT	300
TCTACCCCGT CATTGGATAT AGCTCTGGA GTAGCTCACA GAAATCCTTA CAAATCTTCT	360
GATGAGACTA TATTAGATT ATTACAGTCC GTGCATATTC TTAACATGGA GCCTTACACT	420
TTAGATGAGT CACGTCGCAT GATGGAGTAT TTGGTATCAT CCAACGTTG CCTTGAAAAG	480
GTTGATAATT ATTTGCAAAA TCATGTCCTT AGTGGTGGTA ATCCCGAAA GTTTTTGAT	540
GCTTGCACAC GTCTAGCATG ATTGAGATAT TCAAAAATTT CTATCCACTA CAACTCCTT	600
AACCGGGTTT TATTTTCTA TTTCTATTC TCATGTTGTT CCAAATATGT ATCATCTCGT	660
ATTAGGCTTT TTTCCGTTT ACTCCTGGAA TCGTACCTTT TTCACTATTC CCCCTAATGA	720
ATAATCTAAA TTAGTTTCGC TTATAATTGA TAGTAGTAGA AAGATTGGTG ATTCTACTCG	780
TGTAATGTTA TTAGTTAAA GATACTTGC AAAACATTAA TTAGCTATCA TTATATAAAA	840
AAAATCCTAT AATTATAAAAT ATTAATCAAT ATTTGCGGTC ACTATTATT TAAAACGTTA	900
TGATCAGTAG GACACTTGC ATATATATAG TTATGCTTAA TGGTTACTTG TAACTTGC	958
ATG ACC GAA CAC CAT ACC CCC AAA AGC AGG ATT CTT CGC TTT CTA GAG	1006
Met Thr Glu His His Thr Pro Lys Ser Arg Ile Leu Arg Phe Leu Glu	
1 5 10 15	
AAT CAA TAT GTA TAC CTA TGT ACC TTA AAT GAT TAT GTA CAA CTT GTT	1054
Asn Gln Tyr Val Tyr Leu Cys Thr Leu Asn Asp Tyr Val Gln Leu Val	
20 25 30	
TTG AGA GGG TCG CCG GCA AGC TCG TAT AGC AAT ATA TGC GAA CGC TTG	1102
Leu Arg Gly Ser Pro Ala Ser Ser Tyr Ser Asn Ile Cys Glu Arg Leu	
35 40 45	
AGA AGC GAT GTA CAA ACG TCC TTT TCT ATT TTT CTT CAT TCG ACT GTA	1150
Arg Ser Asp Val Gln Thr Ser Phe Ser Ile Phe Leu His Ser Thr Val	
50 55 60	
GTC GGC TTC GAC AGT AAG CCA GAT GAA GGT GTT CAA TTT TCT TCT CCA	1198
Val Gly Phe Asp Ser Lys Pro Asp Glu Gly Val Gln Phe Ser Ser Pro	
65 70 75 80	
AAA TGC TCA CAG TCA GAG GTATATATAT TTTTGTGTTG ATTTTTCT	1246
Lys Cys Ser Gln Ser Glu	
85	
ATTCGGGATA GCTAATATAT GGGCAG CTA ATA GCG AAT GTT GTA AAA CAG ATG	1299
Leu Ile Ala Asn Val Val Lys Gln Met	
90 95	

TTC GAT GAA AGT TTT GAG CGT CGA AGG AAT CTA CTG ATG AAA GGG TTT Phe Asp Glu Ser Phe Glu Arg Arg Arg Asn Leu Leu Met Lys Gly Phe 100 105 110	1347
TCC ATG GTAAGGTATT CTAATTGTGA AATATTACCG TGCAATTACT GTTTCAAAGA Ser Met	1403
GATTGTATTT AACCGATAAA G AAT CAT GAA GAT TTT CGA GCC ATG CAT GTA Asn His Glu Asp Phe Arg Ala Met His Val 115 120	1454
AAC GGA GTA CAA AAT GAT CTC GTT TCT ACT TTT CCT AAT TAC CTT ATA Asn Gly Val Gln Asn Asp Leu Val Ser Thr Phe Pro Asn Tyr Leu Ile 125 130 135	1502
TCT ATA CTT GAG TCA AAA AAT TGG CAA CTT TTG TTA GAA AT Ser Ile Leu Glu Ser Lys Asn Trp Gln Leu Leu Glu Ile 140 145 150	1543
GTAAATACCG GTTAAGATGT TGCGCACTTT GAACAAGACT GACAAGTATA G T ATC Ile	1598
GGC AGT GAT GCC ATG CAT TAC TTA TTA TCC AAA GGA AGT ATT TTT GAG Gly Ser Asp Ala Met His Tyr Leu Leu Ser Lys Gly Ser Ile Phe Glu 155 160 165 170	1646
GCT CTT CCA AAT GAC AAT TAC CTT CAG ATT TCT GGC ATA CCA CTT TTT Ala Leu Pro Asn Asp Asn Tyr Leu Gln Ile Ser Gly Ile Pro Leu Phe 175 180 185	1694
AAA AAT AAT GTG TTT GAG GAA ACT GTG TCA AAA AAA AGA AAG CGA ACC Lys Asn Asn Val Phe Glu Glu Thr Val Ser Lys Lys Arg Lys Arg Thr 190 195 200	1742
ATT GAA ACA TCC ATT ACT CAA AAT AAA AGC GCC CGC AAA GAA GTT TCC Ile Glu Thr Ser Ile Thr Gln Asn Lys Ser Ala Arg Lys Glu Val Ser 205 210 215	1790
TGG AAT AGC ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC Trp Asn Ser Ile Ser Ile Ser Arg Phe Ser Ile Phe Tyr Arg Ser Ser 220 225 230	1838
TAT AAG AAG TTT AAG CAA G GTAACTAATA CTGTTATCCT TCATAACTAA Tyr Lys Lys Phe Lys Gln 235 240	1887
TTTTAG AT CTA TAT TTT AAC TTA CAC TCT ATT TGT GAT CGG AAC ACA Asp Leu Tyr Phe Asn Leu His Ser Ile Cys Asp Arg Asn Thr 245 250	1934
GTA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG CAA TTT GGA CTT ATA Val His Met Trp Leu Gln Trp Ile Phe Pro Arg Gln Phe Gly Leu Ile 255 260 265 270	1982
AAC GCA TTT CAA GTG AAG CAA TTG CAC AAA GTG ATT CCA CTG GTA TCA Asn Ala Phe Gln Val Lys Gln Leu His Lys Val Ile Pro Leu Val Ser 275 280 285	2030

CAG AGT ACA GTT GTG CCC AAA CGT CTC CTA AAG GTA TAC CCT TTA ATT Gln Ser Thr Val Val Pro Lys Arg Leu Leu Lys Val Tyr Pro Leu Ile 290 295 300	2078
GAA CAA ACA GCA AAG CGA CTC CAT CGT ATT TCT CTA TCA AAA GTT TAC Glu Gln Thr Ala Lys Arg Leu His Arg Ile Ser Leu Ser Lys Val Tyr 305 310 315	2126
AAC CAT TAT TGC CCA TAT ATT GAC ACC CAC GAT GAT GAA AAA ATC CTT Asn His Tyr Cys Pro Tyr Ile Asp Thr His Asp Asp Glu Lys Ile Leu 320 325 330	2174
AGT TAT TCC TTA AAG CCG AAC CAG GTG TTT GCG TTT CTT CGA TCC ATT Ser Tyr Ser Leu Lys Pro Asn Gln Val Phe Ala Phe Leu Arg Ser Ile 335 340 345 350	2222
CTT GTT CGA GTG TTT CCT AAA TTA ATC TGG GGT AAC CAA AGG ATA TTT Leu Val Arg Val Phe Pro Lys Leu Ile Trp Gly Asn Gln Arg Ile Phe 355 360 365	2270
GAG ATA ATA TTA AAA G GTATTGTATA AAATTTATTA CCACTAACGA TTTTACCAAG AC 2327 Glu Ile Ile Leu Lys 370	Asp
CTC GAA ACT TTC TTG AAA TTA TCG AGA TAC GAG TCT TTT AGT TTA CAT Leu Glu Thr Phe Leu Lys Leu Ser Arg Tyr Glu Ser Phe Ser Leu His 375 380 385	2375
TAT TTA ATG AGT AAC ATA AAG GTAATATGCC AAATTTTTT ACCATTAATT Tyr Leu Met Ser Asn Ile Lys 390 395	2426
AACAATCAG ATT TCA GAA ATT GAA TGG CTA GTC CTT GGA AAA AGG TCA Ile Ser Glu Ile Glu Trp Leu Val Leu Gly Lys Arg Ser 400 405	2474
AAT GCG AAA ATG TGC TTA AGT GAT TTT GAG AAA CGC AAG CAA ATA TTT Asn Ala Lys Met Cys Leu Ser Asp Phe Glu Lys Arg Lys Gln Ile Phe 410 415 420	2522
GCG GAA TTC ATC TAC TGG CTA TAC AAT TCG TTT ATA ATA CCT ATT TTA Ala Glu Phe Ile Tyr Trp Leu Tyr Asn Ser Phe Ile Ile Pro Ile Leu 425 430 435 440	2570
CAA TCT TTT TAT ATC ACT GAA TCA AGT GAT TTA CGA AAT CGA ACT Gln Ser Phe Phe Tyr Ile Thr Glu Ser Ser Asp Leu Arg Asn Arg Thr 445 450 455	2618
GTT TAT TTT AGA AAA GAT ATT TGG AAA CTC TTG TGC CGA CCC TTT ATT Val Tyr Phe Arg Lys Asp Ile Trp Lys Leu Leu Cys Arg Pro Phe Ile 460 465 470	2666
ACA TCA ATG AAA ATG GAA GCG TTT GAA AAA ATA AAC GAG GTATTTAAA Thr Ser Met Lys Met Glu Ala Phe Glu Lys Ile Asn Glu 475 480 485	2715
GTATTTTTG CAAAAAGCTA ATATTTCACTAAC AAT GTT AGG ATG GAT ACT CAG Asn Asn Val Arg Met Asp Thr Gln 490	2769

AAA ACT ACT TTG CCT CCA GCA GTT ATT CGT CTA TTA CCT AAG AAG AAT Lys Thr Thr Leu Pro Pro Ala Val Ile Arg Leu Leu Pro Lys Lys Asn 495 500 505	2817
ACC TTT CGT CTC ATT ACG AAT TTA AGA AAA AGA TTC TTA ATA AAG Thr Phe Arg Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu Ile Lys 510 515 520	2862
GTATTAATTT TTGGTCATCA ATGTACTTTA CTTCTAATCT ATTATTAGCA G ATG GGT Met Gly 525	2919
TCA AAC AAA AAA ATG TTA GTC AGT ACG AAC CAA ACT TTA CGA CCT GTG Ser Asn Lys Lys Met Leu Val Ser Thr Asn Gln Thr Leu Arg Pro Val 530 535 540	2967
GCA TCG ATA CTG AAA CAT TTA ATC AAT GAA GAA AGT AGT GGT ATT CCA Ala Ser Ile Leu Lys His Leu Ile Asn Glu Glu Ser Ser Gly Ile Pro 545 550 555	3015
TTT AAC TTG GAG GTT TAC ATG AAG CTT CTT ACT TTT AAG AAG GAT CTT Phe Asn Leu Glu Val Tyr Met Lys Leu Leu Thr Phe Lys Lys Asp Leu 560 565 570	3063
CTT AAG CAC CGA ATG TTT GG GTAATTATAT AATGCGCGAT TCCTCATTAT Leu Lys His Arg Met Phe Gly 575 580	3113
TAATTTTGCA G G CGT AAG AAG TAT TTT GTA CGG ATA GAT ATA AAA TCC Arg Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys Ser 585 590	3161
TGT TAT GAT CGA ATA AAG CAA GAT TTG ATG TTT CGG ATT GTT AAA AAG Cys Tyr Asp Arg Ile Lys Gln Asp Leu Met Phe Arg Ile Val Lys Lys 595 600 605	3209
AAA CTC AAG GAT CCC GAA TTT GTA ATT CGA AAG TAT GCA ACC ATA CAT Lys Leu Lys Asp Pro Glu Phe Val Ile Arg Lys Tyr Ala Thr Ile His 610 615 620 625	3257
GCA ACA AGT GAC CGA GCT ACA AAA AAC TTT GTT AGT GAG GCG TTT TCC Ala Thr Ser Asp Arg Ala Thr Lys Asn Phe Val Ser Glu Ala Phe Ser 630 635 640	3305
TAT T GTAAGTTAT TTTTCATTG GAATTTTTA ACAAATTCTT TTTTAG TT Tyr Phe	3357
GAT ATG GTG CCT TTT GAA AAA GTC GTG CAG TTA CTT TCT ATG AAA ACA Asp Met Val Pro Phe Glu Lys Val Val Gln Leu Leu Ser Met Lys Thr 645 650 655	3405
TCA GAT ACT TTG TTT GTT GAT TTT GTG GAT TAT TGG ACC AAA AGT TCT Ser Asp Thr Leu Phe Val Asp Phe Val Asp Tyr Trp Thr Lys Ser Ser 660 665 670 675	3453
TCT GAA ATT TTT AAA ATG CTC AAG GAA CAT CTC TCT GGA CAC ATT GTT Ser Glu Ile Phe Lys Met Leu Lys Glu His Leu Ser Gly His Ile Val 680 685 690	3501

AAG GTATACCAAT TGTTGAATTG TAATAACACT AATGAAACTA G ATA GGA AAT Lys	Ile Gly Asn	3554
	695	
TCT CAA TAC CTT CAA AAA GTT GGT ATC CCT CAG GGC TCA ATT CTG TCA Ser Gln Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile Leu Ser 700 705 710		3602
TCT TTT TTG TGT CAT TTC TAT ATG GAA GAT TTG ATT GAT GAA TAC CTA Ser Phe Leu Cys His Phe Tyr Met Glu Asp Leu Ile Asp Glu Tyr Leu 715 720 725		3650
TCG TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA GTA GTC GAC GAT Ser Phe Thr Lys Lys Gly Ser Val Leu Leu Arg Val Val Asp Asp 730 735 740		3698
TTC CTC TTT ATA ACA GTT AAT AAA AAG GAT GCA AAA AAA TTT TTG AAT Phe Leu Phe Ile Thr Val Asn Lys Lys Asp Ala Lys Lys Phe Leu Asn 745 750 755		3746
TTA TCT TTA AGA G GTGAGTTGCT GTCATTCCTA AGTTCTAACCGTTGAAG GA Leu Ser Leu Arg Gly 760		3798
TTT GAG AAA CAC AAT TTT TCT ACG AGC CTG GAG AAA ACA GTA ATA AAC Phe Glu Lys His Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile Asn 765 770 775 780		3846
TTT GAA AAT AGT AAT GGG ATA ATA AAC AAT ACT TTT TTT AAT GAA AGC Phe Glu Asn Ser Asn Gly Ile Ile Asn Asn Thr Phe Phe Asn Glu Ser 785 790 795		3894
AAG AAA AGA ATG CCA TTC TTC GGT TTC TCT GTG AAC ATG AGG TCT CTT Lys Lys Arg Met Pro Phe Phe Gly Phe Ser Val Asn Met Arg Ser Leu 800 805 810		3942
GAT ACA TTG TTA GCA TGT CCT AAA ATT GAT GAA GCC TTA TTT AAC TCT Asp Thr Leu Leu Ala Cys Pro Lys Ile Asp Glu Ala Leu Phe Asn Ser 815 820 825		3990
ACA TCT GTA GAG CTG ACG AAA CAT ATG GGG AAA TCT TTT TTT TAC AAA Thr Ser Val Glu Leu Thr Lys His Met Gly Lys Ser Phe Phe Tyr Lys 830 835 840		4038
ATT CTA AG GTATACTGTG TAACTGAATA ATAGCTGACA AATAATCAG A TCG Ile Leu Arg Ser 845		4089
AGC CTT GCA TCC TTT GCA CAA GTA TTT ATT GAC ATT ACC CAC AAT TCA Ser Leu Ala Ser Phe Ala Gln Val Phe Ile Asp Ile Thr His Asn Ser 850 855 860		4137
AAA TTC AAT TCT TGC AAT ATA TAT AGG CTA GGA TAC TCT ATG TGT Lys Phe Asn Ser Cys Cys Asn Ile Tyr Arg Leu Gly Tyr Ser Met Cys 865 870 875 880		4185
ATG AGA GCA CAA GCA TAC TTA AAA AGG ATG AAG GAT ATA TTT ATT CCC Met Arg Ala Gln Ala Tyr Leu Lys Arg Met Lys Asp Ile Phe Ile Pro 885 890 895		4233

CAA AGA ATG TTC ATA ACG G GTGAGTACTT ATTTAACTA GAAAAGTCAT Gln Arg Met Phe Ile Thr 900	4282
TAATTAACCT TAG AT CTT TTG AAT GTT ATT GGA AGA AAA ATT TGG AAA Asp Leu Leu Asn Val Ile Gly Arg Lys Ile Trp Lys 905 910	4330
AAG TTG GCC GAA ATA TTA GGA TAT ACG AGT AGG CGT TTC TTG TCC TCT Lys Leu Ala Glu Ile Leu Gly Tyr Thr Ser Arg Arg Phe Leu Ser Ser 915 920 925 930	4378
GCA GAA GTC AAA TG GTACGTGTCG GTCTCGAGAC TTCAGCAATA TTGACACATC Ala Glu Val Lys Trp 935	4432
AG G CTT TTT TGT CTT GGA ATG AGA GAT GGT TTG AAA CCC TCT TTC AAA Leu Phe Cys Leu Gly Met Arg Asp Gly Leu Lys Pro Ser Phe Lys 940 945 950	4480
TAT CAT CCA TGC TTC GAA CAG CTA ATA TAC CAA TTT CAG TCA TTG ACT Tyr His Pro Cys Phe Glu Gln Leu Ile Tyr Gln Phe Gln Ser Leu Thr 955 960 965	4528
GAT CTT ATC AAG CCG CTA AGA CCA GTT TTG CGA CAG GTG TTA TTT TTA Asp Leu Ile Lys Pro Leu Arg Pro Val Leu Arg Gln Val Leu Phe Leu 970 975 980	4576
CAT AGA AGA ATA GCT GAT TAATGTCATT TTCAATTAT TATATACATC His Arg Arg Ile Ala Asp 985	4624
CTTTATTACT GGTGTCTTAA ACAATATTAT TACTAAGTAT AGCTGACCCC CAAAGCAAGC	4684
ATACTATAGG ATTTCTAGTA AAGTAAAATT AATCTCGTTA TTAGTTTGA TTGACTTGTC	4744
TTTATCCTTA TACTTTAAG AAAGATTGAC AGTGGTTGCT GACTACTGCC CACATGCCA	4804
TTAACACGGGA GTGGTTAAC ATTAAAAGTA ATACATGAGG CTAATCTCCT TTCATTTAGA	4864
ATAAGGAAAG TGGTTTCTA TAATGAATAA TGCCCGCACT AATGCAAAAA GACGAAGATT	4924
ATCTTCTAAA CAAGGGGAT TAAGCATATC CGAAGGAAA GAGAGTAATA TACCCAGTGT	4984
TGTTGAAGAA AGCAAGGATA ATTTGGAACA AGCTTCTGCA GATGACAGGC TAAATTTGG	5044
TGACCGAATT TTGGTAAAG CCCCAGGTTA TCCATGGTGG CCGGCCTTGC TACTGAGACG	5104
AAAAGAAACT AAGGATAGTT TGAATACTAA TAGCTCATT AATGTCTTAT ATAAGGTTT	5164
GTTTTTCCT GACTTCAATT TTGCATGGT GAAAAGAAAT AGTGTAAAGC CATTATTGGA	5224
TTCCGAAATA GCCAAATTTC TTGGTTCTC AAAGCGGAAG TCTAAAGAAC TTATTGAAGC	5284
TTATGAGGCT TCAAAAACTC CTCCTGATTT AAAGGAGGAA TCTTCCACCG ATGAGGAAAT	5344
GGATAGCTTA TCAGCTGCTG AGGAGAAGCC TAATTTTTG CAAAAAAAGAA AATATCATTG	5404
GGAGACATCT CTTGATGAAT CAGATGCGGA GAGTATCTCC AGCGGATCCT TGATGTCAAT	5464
AACTTCTATT TCTGAAATGT ATGGTCCTAC TGTCGCTTCG ACTTCTCGTA GCTCTACGCA	5524

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 988 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met Thr Glu His His Thr Pro Lys Ser Arg Ile Leu Arg Phe Leu Glu
 1 5 10 15

Asn Gln Tyr Val Tyr Leu Cys Thr Leu Asn Asp Tyr Val Gln Leu Val
 20 25 30

Leu Arg Gly Ser Pro Ala Ser Ser Tyr Ser Asn Ile Cys Glu Arg Leu
 35 40 45

Arg Ser Asp Val Gln Thr Ser Phe Ser Ile Phe Leu His Ser Thr Val
 50 55 60

Val Gly Phe Asp Ser Lys Pro Asp Glu Gly Val Gln Phe Ser Ser Pro
 65 70 75 80

Lys Cys Ser Gln Ser Glu Leu Ile Ala Asn Val Val Lys Gln Met Phe
 85 90 95

Asp Glu Ser Phe Glu Arg Arg Asn Leu Leu Met Lys Gly Phe Ser
 100 105 110

Met Asn His Glu Asp Phe Arg Ala Met His Val Asn Gly Val Gln Asn
 115 120 125

Asp Leu Val Ser Thr Phe Pro Asn Tyr Leu Ile Ser Ile Leu Glu Ser
 130 135 140

Lys Asn Trp Gln Leu Leu Glu Ile Ile Gly Ser Asp Ala Met His
 145 150 155 160

Tyr Leu Leu Ser Lys Gly Ser Ile Phe Glu Ala Leu Pro Asn Asp Asn
 165 170 175

Tyr Leu Gln Ile Ser Gly Ile Pro Leu Phe Lys Asn Asn Val Phe Glu
 180 185 190

Glu Thr Val Ser Lys Lys Arg Lys Arg Thr Ile Glu Thr Ser Ile Thr
 195 200 205

Gln Asn Lys Ser Ala Arg Lys Glu Val Ser Trp Asn Ser Ile Ser Ile
 210 215 220

Ser Arg Phe Ser Ile Phe Tyr Arg Ser Ser Tyr Lys Lys Phe Lys Gln
 225 230 235 240

Asp Leu Tyr Phe Asn Leu His Ser Ile Cys Asp Arg Asn Thr Val His
 245 250 255

Met Trp Leu Gln Trp Ile Phe Pro Arg Gln Phe Gly Leu Ile Asn Ala
 260 265 270

 Phe Gln Val Lys Gln Leu His Lys Val Ile Pro Leu Val Ser Gln Ser
 275 280 285

 Thr Val Val Pro Lys Arg Leu Leu Lys Val Tyr Pro Leu Ile Glu Gln
 290 295 300

 Thr Ala Lys Arg Leu His Arg Ile Ser Leu Ser Lys Val Tyr Asn His
 305 310 315 320

 Tyr Cys Pro Tyr Ile Asp Thr His Asp Asp Glu Lys Ile Leu Ser Tyr
 325 330 335

 Ser Leu Lys Pro Asn Gln Val Phe Ala Phe Leu Arg Ser Ile Leu Val
 340 345 350

 Arg Val Phe Pro Lys Leu Ile Trp Gly Asn Gln Arg Ile Phe Glu Ile
 355 360 365

 Ile Leu Lys Asp Leu Glu Thr Phe Leu Lys Leu Ser Arg Tyr Glu Ser
 370 375 380

 Phe Ser Leu His Tyr Leu Met Ser Asn Ile Lys Ile Ser Glu Ile Glu
 385 390 395 400

 Trp Leu Val Leu Gly Lys Arg Ser Asn Ala Lys Met Cys Leu Ser Asp
 405 410 415

 Phe Glu Lys Arg Lys Gln Ile Phe Ala Glu Phe Ile Tyr Trp Leu Tyr
 420 425 430

 Asn Ser Phe Ile Ile Pro Ile Leu Gln Ser Phe Phe Tyr Ile Thr Glu
 435 440 445

 Ser Ser Asp Leu Arg Asn Arg Thr Val Tyr Phe Arg Lys Asp Ile Trp
 450 455 460

 Lys Leu Leu Cys Arg Pro Phe Ile Thr Ser Met Lys Met Glu Ala Phe
 465 470 475 480

 Glu Lys Ile Asn Glu Asn Asn Val Arg Met Asp Thr Gln Lys Thr Thr
 485 490 495

 Leu Pro Pro Ala Val Ile Arg Leu Leu Pro Lys Lys Asn Thr Phe Arg
 500 505 510

 Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu Ile Lys Met Gly Ser Asn
 515 520 525

 Lys Lys Met Leu Val Ser Thr Asn Gln Thr Leu Arg Pro Val Ala Ser
 530 535 540

 Ile Leu Lys His Leu Ile Asn Glu Glu Ser Ser Gly Ile Pro Phe Asn
 545 550 555 560

 Leu Glu Val Tyr Met Lys Leu Leu Thr Phe Lys Lys Asp Leu Leu Lys
 565 570 575

His Arg Met Phe Gly Arg Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys
 580 585 590
 Ser Cys Tyr Asp Arg Ile Lys Gln Asp Leu Met Phe Arg Ile Val Lys
 595 600 605
 Lys Lys Leu Lys Asp Pro Glu Phe Val Ile Arg Lys Tyr Ala Thr Ile
 610 615 620
 His Ala Thr Ser Asp Arg Ala Thr Lys Asn Phe Val Ser Glu Ala Phe
 625 630 635 640
 Ser Tyr Phe Asp Met Val Pro Phe Glu Lys Val Val Gln Leu Leu Ser
 645 650 655
 Met Lys Thr Ser Asp Thr Leu Phe Val Asp Phe Val Asp Tyr Trp Thr
 660 665 670
 Lys Ser Ser Ser Glu Ile Phe Lys Met Leu Lys Glu His Leu Ser Gly
 675 680 685
 His Ile Val Lys Ile Gly Asn Ser Gln Tyr Leu Gln Lys Val Gly Ile
 690 695 700
 Pro Gln Gly Ser Ile Leu Ser Ser Phe Leu Cys His Phe Tyr Met Glu
 705 710 715 720
 Asp Leu Ile Asp Glu Tyr Leu Ser Phe Thr Lys Lys Lys Gly Ser Val
 725 730 735
 Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile Thr Val Asn Lys Lys
 740 745 750
 Asp Ala Lys Lys Phe Leu Asn Leu Ser Leu Arg Gly Phe Glu Lys His
 755 760 765
 Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile Asn Phe Glu Asn Ser
 770 775 780
 Asn Gly Ile Ile Asn Asn Thr Phe Phe Asn Glu Ser Lys Lys Arg Met
 785 790 795 800
 Pro Phe Phe Gly Phe Ser Val Asn Met Arg Ser Leu Asp Thr Leu Leu
 805 810 815
 Ala Cys Pro Lys Ile Asp Glu Ala Leu Phe Asn Ser Thr Ser Val Glu
 820 825 830
 Leu Thr Lys His Met Gly Lys Ser Phe Phe Tyr Lys Ile Leu Arg Ser
 835 840 845
 Ser Leu Ala Ser Phe Ala Gln Val Phe Ile Asp Ile Thr His Asn Ser
 850 855 860
 Lys Phe Asn Ser Cys Cys Asn Ile Tyr Arg Leu Gly Tyr Ser Met Cys
 865 870 875 880
 Met Arg Ala Gln Ala Tyr Leu Lys Arg Met Lys Asp Ile Phe Ile Pro
 885 890 895

Gln Arg Met Phe Ile Thr Asp Leu Leu Asn Val Ile Gly Arg Lys Ile
 900 905 910
 Trp Lys Lys Leu Ala Glu Ile Leu Gly Tyr Thr Ser Arg Arg Phe Leu
 915 920 925
 Ser Ser Ala Glu Val Lys Trp Leu Phe Cys Leu Gly Met Arg Asp Gly
 930 935 940
 Leu Lys Pro Ser Phe Lys Tyr His Pro Cys Phe Glu Gln Leu Ile Tyr
 945 950 955 960
 Gln Phe Gln Ser Leu Thr Asp Leu Ile Lys Pro Leu Arg Pro Val Leu
 965 970 975
 Arg Gln Val Leu Phe Leu His Arg Arg Ile Ala Asp
 980 985

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (ix) FEATURE:
 - (A) NAME/KEY: modified_base
 - (B) LOCATION: 1
 - (D) OTHER INFORMATION: /mod_base= OTHER
 /note= "N = guanosine modified by a biotin group"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

NCCTATTTYT TYTAYNNNAC NGA

23

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Phe Phe Tyr Xaa Thr Glu
 1 5

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

CCAGATATNA DNARRAARTC RTC

23

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe, Ile or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Asp Asp Phe Leu Xaa Ile
1 5

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

ACAATGMGNH TNHTNCCNAA RAA

23

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 2..3
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Arg Xaa Xaa Pro Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

ACGAATCKNG GDATNSWRG RTARCA

26

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Cys Tyr Asp Ser Ile Pro Arg
1 5

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CAATTCTCRT ARCANSWYTT DATRTC

26

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Asp Ile Lys Ser Cys Tyr Asp
1 5

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GATTACTCCC GAAGAAAGGA TCTTTCCGTC CAATCATGAC TTTCTTAAGA AAGGACAAGC	60
AAAAAAATAT TAAGTTAAAT CTAAATTAAA TTCTAATGGA TAGCCAACCT GTGTTTAGGA	120
ATTTAAAAGA CATGCTGGGA TAAAAGATAG GATACTCAGT CTTTGATAAT AAACAAATT	180
CAGAAAAATT TGCCTAATTC ATAGAGAAAT GGAAAATAA AGGAAGACCT CAGCTATATT	240
ATGTCACTCT AGACATAAAG ACTTGCTAC	269

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

AAACACAAAGG AAGGAAGTCA AATATTCTAT TACCGTAAAC CAATATGGAA ATTAGTGAGT	60
AAATTAACTA TTGTCAAAGT AAGAATTAG TTTCTGAAA AGAATAAATA AATGAAAAAT	120
AATTTTATC AAAAAATTG GCTTGAAGAG GAGAATTGAG AAAAAAGTTGA AGAAAAATTG	180
ATACCAGAAG ATTCATTTA GAAATACCT CAAGGAAAGC TAAGGATTAT ACCTAAAAAA	240
GGATCTTCC GTCCAATCAT GACTTCTTA AGAAAGGACA AGCAAAAAAA TATTAAGTTA	300
AATCTAAATT AAATTCTAAT GGATAGCCAA CTTGTGTTA GGAATTAAA AGACATGCTG	360
GGATAAAAGA TAGGATACTC AGTCTTGAT AATAAACAAA TTTCAGAAAA ATTTGCCTAA	420
TTCATAGAGA AATGGAAAAA TAAAGGAAGA CCTCAGCTAT ATTATGTCAC TCTA	474

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Ala Tyr Asp Thr Ile
1 5

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Phe Phe Tyr Cys Thr Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe
1 5 10 15

Arg His Asp Thr Trp Asn Lys Leu Ile Thr Pro Phe Ile Val Glu Tyr
20 25 30

Phe Lys Thr Tyr Leu Val Glu Asn Asn Val Cys Arg Asn His Asn Ser
35 40 45

Tyr Thr Leu Ser Asn Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys
50 55 60

Lys Ser Asn Asn Glu Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala
65 70 75 80

Asp Glu Glu Glu Phe Thr Ile Tyr Lys Glu Asn His Lys Asn Ala Ile
85 90 95

Gln Pro Thr Gln Lys Ile Leu Glu Tyr Leu Arg Asn Lys Arg Pro Thr
100 105 110

Ser Phe Thr Lys Ile Tyr Ser Pro Thr Gln Ile Ala Asp Arg Ile Lys
115 120 125

Glu Phe Lys Gln Arg Leu Leu Lys Lys Phe Asn Asn Val Leu Pro Glu
130 135 140

Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr Asp
145 150 155

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr Tyr
1 5 10 15

Tyr Arg Lys Asn Ile Trp Asp Val Ile Met Lys Met Ser Ile Ala Asp
20 25 30

Leu Lys Lys Glu Thr Leu Ala Glu Val Gln Glu Lys Glu Val Glu Glu
35 40 45

Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly Lys Leu Arg Leu Ile Pro
50 55 60

Lys Lys Thr Thr Phe Arg Pro Ile Met Thr Phe Asn Lys Lys Ile Val
65 70 75 80

Asn	Ser	Asp	Arg	Lys	Thr	Thr	Lys	Leu	Thr	Thr	Asn	Thr	Lys	Leu	Leu
				85					90				95		
Asn	Ser	His	Leu	Met	Leu	Lys	Thr	Leu	Lys	Asn	Arg	Met	Phe	Lys	Asp
				100				105				110			
Pro	Phe	Gly	Phe	Ala	Val	Phe	Asn	Tyr	Asp	Asp	Val	Met	Lys	Lys	Tyr
				115				120				125			
Glu	Glu	Phe	Val	Cys	Lys	Trp	Lys	Gln	Val	Gly	Gln	Pro	Lys	Leu	Phe
				130			135				140				
Phe	Ala	Thr	Met	Asp	Ile	Glu	Lys	Cys	Tyr	Asp					
				145		150				155					

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Lys	His	Lys	Glu	Gly	Ser	Gln	Ile	Phe	Tyr	Tyr	Arg	Lys	Pro	Ile	Trp
1				5					10					15	
Lys	Leu	Val	Ser	Lys	Leu	Thr	Ile	Val	Lys	Val	Arg	Ile	Gln	Phe	Ser
				20				25					30		
Glu	Lys	Asn	Lys	Gln	Met	Lys	Asn	Asn	Phe	Tyr	Gln	Lys	Ile	Gln	Leu
				35			40				45				
Glu	Glu	Glu	Asn	Leu	Glu	Lys	Val	Glu	Glu	Lys	Leu	Ile	Pro	Glu	Asp
				50		55				60					
Ser	Phe	Gln	Lys	Tyr	Pro	Gln	Gly	Lys	Leu	Arg	Ile	Ile	Pro	Lys	Lys
				65		70			75				80		
Gly	Ser	Phe	Arg	Pro	Ile	Met	Thr	Phe	Leu	Arg	Lys	Asp	Lys	Gln	Lys
					85			90				95			
Asn	Ile	Lys	Leu	Asn	Leu	Asn	Gln	Ile	Leu	Met	Asp	Ser	Gln	Leu	Val
				100				105				110			
Phe	Arg	Asn	Leu	Lys	Asp	Met	Leu	Gly	Gln	Lys	Ile	Gly	Tyr	Ser	Val
				115			120				125				
Phe	Asp	Asn	Lys	Gln	Ile	Ser	Glu	Lys	Phe	Ala	Gln	Phe	Ile	Glu	Lys
				130		135				140					
Trp	Lys	Asn	Lys	Gly	Arg	Pro	Gln	Leu	Tyr	Tyr	Val	Thr	Leu		
				145			150				155				

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Gly Ile Pro Gln Gly
1 5

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GTGAAGGCAC TGTTCAGCG

19

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GTGGATGATT TCTTGTTGG

19

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

ATGCTCCTGC GTTTGGTGG

19

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CTGGACACTC AGCCCTTGG

19

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GGCAGGTGTG CTGGACACT

19

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

TTTGATGATG CTGGCGATG

19

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GGGGCTCGTC TTCTACAGG

19

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CAGCAGGAGG ATCTTGTAG

19

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TGACCCCAGG AGTGGCACG

19

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

TCAAGCTGAC TCGACACCG

19

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CGGCGTGACA GGGCTGC

17

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GCTGAAGGCT GAGTGTCC

18

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TAGTCCATGT TCACAATCG

19

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 22.1716

(D) OTHER INFORMATION: /note= "DNA encoding ORF for 63 kD hTRT protein from EcoRI-NotI insert of clone 712562"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GCCAAGTTCC	TGC	ACTGGCT	G	ATG	AGT	GTG	TAC	GTC	GTC	GAG	CTG	CTC	AGG	51	
				Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg		
				1					5				10		
TCT	TTC	TTT	TAT	GTC	ACG	GAG	ACC	ACG	TTT	CAA	AAG	AAC	AGG	CTC	TTT
Ser	Phe	Phe	Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe
	15				20					25					99
TTC	TAC	CGG	AAG	AGT	GTC	TGG	AGC	AAG	TTG	CAA	AGC	ATT	GGA	ATC	AGA
Phe	Tyr	Arg	Lys	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	Arg
	30				35					40					147
CAG	CAC	TTG	AAG	AGG	GTG	CAG	CTG	CGG	GAG	CTG	TCG	GAA	GCA	GAG	GTC
Gln	His	Leu	Lys	Arg	Val	Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu	Val
	45				50					55					195
AGG	CAG	CAT	CGG	GAA	GCC	AGG	CCC	GCC	CTG	CTG	ACG	TCC	AGA	CTC	CGC
Arg	Gln	His	Arg	Glu	Ala	Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu	Arg
	60				65					70					243
TTC	ATC	CCC	AAG	CCT	GAC	GGG	CTG	CGG	CCG	ATT	GTG	AAC	ATG	GAC	TAC
Phe	Ile	Pro	Lys	Pro	Asp	Gly	Leu	Arg	Pro	Ile	Val	Asn	Met	Asp	Tyr
	75				80				85					90	
GTC	GTG	GGA	GCC	AGA	ACG	TTC	CGC	AGA	GAA	AAG	ARG	GCC	GAG	CGT	CTC
Val	Val	Gly	Ala	Arg	Thr	Phe	Arg	Arg	Glu	Lys	Xaa	Ala	Glu	Arg	Leu
	95					100					105				339
ACC	TCG	AGG	GTG	AAG	GCA	CTG	TTC	AGC	GTG	CTC	AAC	TAC	GAG	CGG	GCG
Thr	Ser	Arg	Val	Lys	Ala	Leu	Phe	Ser	Val	Leu	Asn	Tyr	Glu	Arg	Ala
	110				115					120					387
CGG	CGC	CCC	GGC	CTC	CTG	GGC	GCC	TCT	GTG	CTG	GGC	CTG	GAC	GAT	ATC
Arg	Arg	Pro	Gly	Leu	Leu	Gly	Ala	Ser	Val	Leu	Gly	Leu	Asp	Asp	Ile
	125				130					135					435
CAC	AGG	GCC	TGG	CGC	ACC	TTC	GTG	CTG	CGT	GTG	CGG	GCC	CAG	GAC	CCG
His	Arg	Ala	Trp	Arg	Thr	Phe	Val	Leu	Arg	Val	Arg	Ala	Gln	Asp	Pro
	140				145					150					483
CCG	CCT	GAG	CTG	TAC	TTT	GTC	AAG	GTG	GAT	GTG	ACG	GGC	GCG	TAC	GAC
Pro	Pro	Glu	Leu	Tyr	Phe	Val	Lys	Val	Asp	Val	Thr	Gly	Ala	Tyr	Asp
	155				160				165					170	
ACC	ATC	CCC	CAG	GAC	AGG	CTC	ACG	GAG	GTC	ATC	GCC	AGC	ATC	ATC	AAA
Thr	Ile	Pro	Gln	Asp	Arg	Leu	Thr	Glu	Val	Ile	Ala	Ser	Ile	Ile	Lys
	175				180					185					579
CCC	CAG	AAC	ACG	TAC	TGC	GTG	CGT	CGG	TAT	GCC	GTG	GTC	CAG	AAG	GCC
Pro	Gln	Asn	Thr	Tyr	Cys	Val	Arg	Arg	Tyr	Ala	Val	Val	Gln	Lys	Ala
	190				195					200					627

GCC ATG GGC ACG TCC GCA AGG CCT TCA AGA GCC ACG TCC TAC GTC CAG Ala Met Gly Thr Ser Ala Arg Pro Ser Arg Ala Thr Ser Tyr Val Gln 205 210 215	675
TGC CAG GGG ATC CCG CAG GGC TCC ATC CTC TCC ACG CTG CTC TGC AGC Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser 220 225 230	723
CTG TGC TAC GGC GAC ATG GAG AAC AAG CTG TTT GCG GGG ATT CGG CGG Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg 235 240 245 250	771
GAC GGG CTG CTC CTG CGT TTG GTG GAT GAT TTC TTG TTG GTG ACA CCT Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro 255 260 265	819
CAC CTC ACC CAC GCG AAA ACC TTC CTC AGG ACC CTG GTC CGA GGT GTC His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val 270 275 280	867
CCT GAG TAT GGC TGC GTG GTG AAC TTG CGG AAG ACA GTG GTG AAC TTC Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe 285 290 295	915
CCT GTA GAA GAC GAG GCC CTG GGT GGC ACG GCT TTT GTT CAG ATG CCG Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro 300 305 310	963
GCC CAC GGC CTA TTC CCC TGG TGC GGC CTG CTG CTG GAT ACC CGG ACC Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr 315 320 325 330	1011
CTG GAG GTG CAG AGC GAC TAC TCC AGC TAT GCC CGG ACC TCC ATC AGA Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg 335 340 345	1059
GCC AGT CTC ACC TTC AAC CGC GGC TTC AAG GCT GGG AGG AAC ATG CGT Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg 350 355 360	1107
CGC AAA CTC TTT GGG GTC TTG CGG CTG AAG TGT CAC AGC CTG TTT CTG Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu 365 370 375	1155
GAT TTG CAG GTG AAC AGC CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys 380 385 390	1203
ATC CTC CTG CTG CAG GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu 395 400 405 410	1251
CCA TTT CAT CAG CAA GTT TGG AAG AAC CCA CAT TTT TCC TGC GCG TCA Pro Phe His Gln Gln Val Trp Lys Asn Pro His Phe Ser Cys Ala Ser 415 420 425	1299
TCT CTG ACA CGG CTC CCT CTG CTA CTC CAT CCT GAA AGC CAA GAA CGC Ser Leu Thr Arg Leu Pro Leu Leu His Pro Glu Ser Gln Glu Arg 430 435 440	1347

AGG GAT GTC GCT GGG GGC CAA GGG CGC CGC CGG CCC TCT GCC CTC CGA Arg Asp Val Ala Gly Gly Gln Gly Arg Arg Arg Pro Ser Ala Leu Arg 445 450 455	1395
GGC CGT GCA GTG GCT GTG CCA CCA AGC ATT CCT GCT CAA GCT GAC TCG Gly Arg Ala Val Ala Val Pro Pro Ser Ile Pro Ala Gln Ala Asp Ser 460 465 470	1443
ACA CCG TGT CAC CTA CGT GCC ACT CCT GGG GTC ACT CAG GAC AGC CCA Thr Pro Cys His Leu Arg Ala Thr Pro Gly Val Thr Gln Asp Ser Pro 475 480 485 490	1491
GAC GCA GCT GAG TCG GAA GCT CCC GGG GAC GAC GCT GAC TGC CCT GGA Asp Ala Ala Glu Ser Glu Ala Pro Gly Asp Asp Ala Asp Cys Pro Gly 495 500 505	1539
GGC CGC AGC CAA CCC GGC ACT GCC CTC AGA CTT CAA GAC CAT CCT GGA Gly Arg Ser Gln Pro Gly Thr Ala Leu Arg Leu Gln Asp His Pro Gly 510 515 520	1587
CTG ATG GCC ACC CGC CCA CAG CCA GGC CGA GAG CAG ACA CCA GCA GCC Leu Met Ala Thr Arg Pro Gln Pro Gly Arg Glu Gln Thr Pro Ala Ala 525 530 535	1635
CTG TCA CGC CGG GCT TAT ACG TCC CAG GGA GGG AGG GGC GGC CCA CAC Leu Ser Arg Arg Ala Tyr Thr Ser Gln Gly Gly Arg Gly Pro His 540 545 550	1683
CCA GGC CTG CAC CGC TGG GAG TCT GAG GCC TGAGTGAGTG TTTGGCCGAG Pro Gly Leu His Arg Trp Glu Ser Glu Ala 555 560	1733
GCCTGCATGT CCGGCTGAAG GCTGAGTGTC CGGCTGAGGC CTGAGCGAGT GTCCAGCCAA	1793
GGGCTGAGTG TCCAGCACAC CTGCGTTTC ACTTCCCCAC AGGCTGGCGT TCGGTCCACC	1853
CCAGGGCCAG CTTTCCTCA CCAGGAGCCC GGCTTCCACT CCCCCACATAG GAATAGTCCA	1913
TCCCCAGATT CGCCATTGTT CACCCTTCGC CCTGCCTTCC TTTGCCTTCC ACCCCCACCA	1973
TTCAGGTGGA GACCCTGAGA AGGACCCTGG GAGCTTGGG AATTTGGAGT GACCAAAGGT	2033
GTGCCCTGTA CACAGGCGAG GACCCTGCAC CTGGATGGGG GTCCCTGTGG GTCAAATTGG	2093
GGGGAGGTGC TGTGGGAGTA AAATACTGAA TATATGAGTT TTTCAGTTT GGAAAAAAA	2153
AAAAAAAAAA AAAAAAAA	2171

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 564 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr
1 5 10 15

Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val
20 25 30

Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val
35 40 45

Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu Ala
50 55 60

Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp
65 70 75 80

Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr
85 90 95

Phe Arg Arg Glu Lys Xaa Ala Glu Arg Leu Thr Ser Arg Val Lys Ala
100 105 110

Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu
115 120 125

Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr
130 135 140

Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr Phe
145 150 155 160

Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg
165 170 175

Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys
180 185 190

Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala Met Gly Thr Ser Ala
195 200 205

Arg Pro Ser Arg Ala Thr Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln
210 215 220

Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met
225 230 235 240

Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg
245 250 255

Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys
260 265 270

Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val
275 280 285

Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala
290 295 300

Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro
305 310 315 320

Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp
 325 330 335
 Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn
 340 345 350
 Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val
 355 360 365
 Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser
 370 375 380
 Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala
 385 390 395 400
 Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val
 405 410 415
 Trp Lys Asn Pro His Phe Ser Cys Ala Ser Ser Leu Thr Arg Leu Pro
 420 425 430
 Leu Leu Leu His Pro Glu Ser Gln Glu Arg Arg Asp Val Ala Gly Gly
 435 440 445
 Gln Gly Arg Arg Arg Pro Ser Ala Leu Arg Gly Arg Ala Val Ala Val
 450 455 460
 Pro Pro Ser Ile Pro Ala Gln Ala Asp Ser Thr Pro Cys His Leu Arg
 465 470 475 480
 Ala Thr Pro Gly Val Thr Gln Asp Ser Pro Asp Ala Ala Glu Ser Glu
 485 490 495
 Ala Pro Gly Asp Asp Ala Asp Cys Pro Gly Gly Arg Ser Gln Pro Gly
 500 505 510
 Thr Ala Leu Arg Leu Gln Asp His Pro Gly Leu Met Ala Thr Arg Pro
 515 520 525
 Gln Pro Gly Arg Glu Gln Thr Pro Ala Ala Leu Ser Arg Arg Ala Tyr
 530 535 540
 Thr Ser Gln Gly Gly Arg Gly Pro His Pro Gly Leu His Arg Trp
 545 550 555 560
 Glu Ser Glu Ala

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CCAGTGAGCA GAGTGACGAG GACTCGAGCT CAAGCTTTT TTTTTTTTT

50

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

CCAGTGAGCA GAGTGACG

18

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GAGGACTCGA GCTCAAGC

18

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CACTGATCCT TTCTTTTCG TAAACGATAG GT

32

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CATCAATCAA ATCTTCCATA TAGAAATGAC A

31

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /mod_base= OTHER
/note= "N = 5' phosphorylated guanosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

NGGCCGTGTT GGCCTAGTTC TCTGCTC

27

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GAGGAGGAGA AGAGCAGAGA ACTAGGCCAA CACGCC

38

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GTGTCATTTC TATATGGAAG ATTTGATTGA TG

32

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

ACCTATCGTT TACGAAAAAG AAAGGATCAG TG

32

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GAGTGACATA ATATACGTGA

20

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Phe Phe Tyr Val Thr Glu
1 5

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4029 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..4029
(D) OTHER INFORMATION: /note= "preliminary sequence of hTRT cDNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

GCAGCGCTGC	GTCCTGCTGC	GCACGTGGGA	AGCCCTGGCC	CCGGCCACCC	CCGCGATGCC	60
GCGCGCTCCC	CGCTGCCGAG	CCGTGCGCTC	CCTGCTGCGC	AGCCACTACC	GCGAGGTGCT	120
GCCGCTGGCC	ACGTCGTGC	GGCGCCTGGG	GCCCCAGGGC	TGGCGGCTGG	TGCAGCGCGG	180
GGACCCGGCG	GCTTCCGCG	CGNTGGTGGC	CCANTGCNTG	GTGTGCGTGC	CCTGGGANGN	240
ANGGCNGCCC	CCCGCCGCC	CCTCCTTCCG	CCAGGTGTCC	TGCCTGAANG	ANCTGGTGGC	300
CCGAGTGCTG	CANANGCTGT	GCGANCAGGG	CGCGAANAAC	GTGCTGGCCT	TCGGCTTCGC	360
GCTGCTGGAC	GGGGCCCGCG	GGGGCCCCCCC	CGAGGCCCTTC	ACCACCAAGCG	TGCCAGCTA	420
CCTGCCAAC	ACGGTGACCG	ACGCACTGCG	GGGGAGCGGG	GCGTGGGGC	TGCTGCTGCG	480
CCGCGTGGGC	GACGACGTGC	TGGTTCACCT	GCTGGCACGC	TGCGCGNTNT	TTGTGCTGGT	540
GGNTCCCAGC	TGCGCCTACC	ANGTGTGCGG	GCCGCCGCTG	TACCAGCTCG	GCGCTGCNAC	600
TCAGGCCCCG	CCCCCGCCAC	ACGCTANTGG	ACCGAANGC	GTCTGGGATC	CAACGGGCCT	660
GGAACCATAG	CGTCAGGGAG	GCCGGGGTCC	CCCTGGGCTG	CCAGCCCCGG	GTGCGAGGAG	720
GCGCGGGGGC	AGTGCCAGCC	GAAGTCTGCC	GTTGCCAAG	AGGCCCAGGC	GTGGCGCTGC	780
CCCTGAGCCG	GAGCGGACGC	CCGTTGGCA	GGGGTCTGG	GCCCACCCGG	GCAGGACGCC	840
TGGACCGAGT	GACCGTGGTT	TCTGTGTGGT	GTCACCTGCC	AGACCCGGC	AAGAAGCCAC	900
CTCTTGGAG	GGTGCCTCT	CTGGCACGCG	CCACTCCCAC	CCATCCGTGG	GCCGCCAGCA	960
CCACCGGGC	CCCCCATCCA	CATCGCGGCC	ACCACGTCT	GGGACACGCC	TTGTCCCCCG	1020
GTGTACGCCG	AGACCAAGCA	CTTCCTCTAC	TCCTCAGGCG	ACAAGNACAC	TGCGNCCCTC	1080
CTTCCTACTC	AATATATCTG	AGGCCAGGCC	TGACTGGCGT	TCGGGAGGTT	CGTGGAGACA	1140
NTCTTCTGG	TTCCAGGCCT	TGGATGCCAG	GATTCCCCGC	AGGTTGCC	GCCTGCCCA	1200
GCGNTACTGG	CAAATGCCGC	CCCTGTTCT	GGAGCTGCTT	GGGAACCACG	CGCAGTGC	1260
CTACGGGTG	TTCCTCAAGA	CGCACTGCC	GCTGCGAGCT	GCGGTACCC	CAGCAGCCGG	1320
TGTCTGTGCC	CGGGAGAAGC	CCCAGGGCTC	TGTGGCGGCC	CCCGAGGAGG	AGGAACACAG	1380
ACCCCCGTG	CCTGGTGCAG	CTGCTCCGCC	AGCACAGCAG	CCCCTGGCAG	GTGTACGGCT	1440
TCGTGCGGGC	CTGCCTGCGC	CGGCTGGTGC	CCCCAGGCCT	CTGGGGCTCC	AGGCACAACG	1500
AACGCCGCTT	CCTCAGGAAC	ACCAAGAAGT	TCATCTCCCT	GGGAAAGCAT	GCCAAGCTCT	1560

CGCTGCAGGA	GCTGACGTGG	AAGATGAGCG	TGCGGGACTG	CGCTTGGCTG	CGCAGGAGCC	1620
CAGGGGTTGG	CTGTGTTCCG	GCCGCAGAGC	ACCGTCTGCG	TGAGGAGATC	CTGGCCAAGT	1680
TCCTGCACTG	GCTGATGAGT	GTGTACGTGCG	TCGAGCTGCT	CAGGTCTTTC	TTTTATGTCA	1740
CGGAGACCAC	GTTTCAAAAG	AACAGGCTCT	TTTTCTACCG	GAAGAGTGTC	TGGAGCAAGT	1800
TGCAAAGCAT	TGGAATCAGA	CAGCACTTGA	AGAGGGTGCA	GCTGCGGGAG	CTGTCGGAAG	1860
CAGAGGTCAG	GCAGCATCGG	GAAGCCAGGC	CCGCCCTGCT	GACGTCCAGA	CTCCGCTTCA	1920
TCCCCAAGCC	TGACGGGCTG	CGGCCGATTG	TGAACATGGA	CTACGTCGTG	GGAGGCCAGAA	1980
CGTTCCGCAG	AGAAAAGAGG	GCCGAGCGTC	TCACCTCGAG	GGTGAAGGCA	CTGTTCAGCG	2040
TGCTCAACTA	CGAGCGGGCG	CGGCGCCCCG	GCCTCCTGGG	CGCCTCTGTG	CTGGGCCTGG	2100
ACGATATCCA	CAGGGCCTGG	CGCACCTTCG	TGCTGCGTGT	GCAGGCCCCAG	GACCCGCCGC	2160
CTGAGCTGTA	CTTTGTCAAG	GTGGATGTGA	CGGGCGCGTA	CGACACCATC	CCCCAGGACA	2220
GGCTCACGGA	GGTCATCGCC	AGCATCATCA	AACCCCAGAA	CACGTACTGC	GTGCGTCGGT	2280
ATGCCGTGGT	CCAGAAGGCC	GCCCATGGGC	ACGTCCGCAA	GGCCTTCAAG	AGCCACGTCT	2340
CTACCTTGAC	AGACCTCCAG	CCGTACATGC	GACAGTTCGT	GGCTCACCTG	CAGGANAACA	2400
GCCCGCTGAG	GGATGCCGTC	GTCATCGAGC	AGAGCTCCTC	CCTGAATGAG	GCCAGCAGTG	2460
GCCTCTTCGA	CGTCTTCCTA	CGCTTCATGT	GCCACCACGC	CGTGCACATC	AGGGGCAAGT	2520
CCTACGTCCA	GTGCCAGGGG	ATCCCGCAGG	GCTCCATCCT	CTCCACGCTG	CTCTGCAGCC	2580
TGTGCTACGG	CGACATGGAG	AACAAGCTGT	TTGCGGGAT	TCGGCGGGAC	GGGCTGCTCC	2640
TGCGTTGGT	GGATGATTTC	TTGTTGGTGA	CACCTCACCT	CACCCACGCG	AAAACCTTCC	2700
TCAGGACCCCT	GGTCCGAGGT	GTCCCTGAGT	ATGGCTGCGT	GGTGAACTTG	CGGAAGACAG	2760
TGGTGAACTT	CCCTGTAGAA	GACGAGGCC	TGGGTGGCAC	GGCTTTGTT	CAGATGCCGG	2820
CCCACGGCCT	ATTCCCCTGG	TGCGGCCTGC	TGCTGGATAC	CCGGACCCCTG	GAGGTGCAGA	2880
GCGACTACTC	CAGCTATGCC	CGGACCTCCA	TCAGAGCCAG	TCTCACCTTC	AACCGCGGCT	2940
TCAAGGCTGG	GAGGAACATG	CGTCGCAAAC	TCTTGGGGT	CTTGCAGCTG	AAGTGTACAA	3000
GCCTGTTCT	GGATTGCA	GTGAACAGCC	TCCAGACGGT	GTGCACCAAC	ATCTACAAGA	3060
TCCTCCTGCT	GCAGGGTAC	AGGTTCACTG	CATGTGTGCT	GCAGCTCCCA	TTTCATCAGC	3120
AAGTTTGGAA	GAACCCCACA	TTTTCCCTGC	CGTCATCTC	TGACACGGCC	TCCCTCTGCT	3180
ACTCCATCCT	GAAAGCCAAG	AACGCAGGGA	TGTCGCTGGG	GGCCAAGGGC	GCCGCCGGCC	3240
CTCTGCCCTC	CGAGGCCGTG	CAGTGGCTGT	GCCACCAAGC	ATTCCCTGCTC	AAGCTGACTC	3300
GACACCGTGT	CACCTACGTG	CCACTCCTGG	GGTCACTCAG	GACAGCCAG	ACGCAGCTGA	3360
GTCGGAAGCT	CCCAGGGACG	ACGCTGACTG	CCCTGGAGGC	CGCAGCCAAC	CCGGCACTGC	3420

CCTCAGACTT CAAGACCATC CTGGACTGAT GGCCACCCGC CCACAGCCAG GCCGAGAGCA	3480
GACACCAGCA GCCCTGTCAC GCCGGGCTCT ACGTCCCAGG GAGGGAGGGG CGGCCACAC	3540
CCAGGCCCGC ACCGCTGGGA GTCTGAGGCC TGAGTGAGTG TTTGGCCGAG GCCTGCATGT	3600
CCGGCTGAAG GCTGAGTGTC CGGCTGAGGC CTGAGCGAGT GTCCAGCCAA GGGCTGAGTG	3660
TCCAGCACAC CTGCCGTCTT CACTTCCCCA CAGGCTGGCG CTCGGCTCCA CCCCAGGGCC	3720
AGCTTTCTT CACCAGGAGC CGGGCTTCCA CTCCCCACAT AGGAATAGTC CATCCCCAGA	3780
TTCGCCATTG TTCACCCCTC GCCCTGCCCT CCTTTGCCTT CCACCCCCAC CATCCAGGTG	3840
GAGACCTGTA GAAGGACCCCT GGGAGCTCTG GGAATTTGGA GTGACCAAAG GTGTGCCCTG	3900
TACACAGGCG AGGACCCCTGC ACCTGGATGG GGGTCCCTGT GGGTCAAATT GGGGGGAGGT	3960
GCTGTGGGAG TAAAATACTG AATATATGAG TTTTCAGTT TTGAAAAAAA AAAAAAAA	4020
AAAAAAAAAA	4029

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Arg or Lys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Val"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 8
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 10
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 11
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Ile or Val"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 12
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Thr or Ser"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Xaa Xaa Xaa Xaa Xaa Asp Asp Xaa Leu Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 18
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 22
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Lys Xaa Tyr Xaa Gln Xaa Xaa Gly Ile Pro Gln Gly Ser Xaa Leu Ser
1 5 10 15
Xaa Xaa Leu Xaa Xaa Xaa Tyr Xaa Asp Leu
20 25

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 8
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 13
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid,
selected from Gly, Ser, Thr, Tyr, Cys,
Asn or Gln"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 21
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid,
selected from Gly, Ser, Thr, Tyr, Cys,
Asn or Gln"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 25
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid,
selected from Gly, Ser, Thr, Tyr, Cys,
Asn or Gln"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Trp	Leu	Xaa	Tyr	Xaa	Phe	Phe	Tyr							
1				5					10					15
Xaa Thr Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Arg Lys														
20 25 30														
Xaa Xaa Trp														
35														

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4038 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 56..3454
(D) OTHER INFORMATION: /note= "refined hTRT DNA sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GCAGCGCTGC	GTCCTGCTGC	GCACGTGGGA	AGCCCTGGCC	CCGGCCACCC	CCGCG	ATG	58									
						Met										
						1										
CCG	CGC	GCT	CCC	CGC	TGC	CGA	GCC	GTG	CGC	TCC	CTG	CTG	CGC	AGC	CAC	106
Pro	Arg	Ala	Pro	Arg	Cys	Arg	Ala	Val	Arg	Ser	Leu	Leu	Arg	Ser	His	
			5				10						15			
TAC	CGC	GAG	GTG	CTG	CCG	CTG	GCC	ACG	TTC	GTG	CGG	CGC	CTG	GGG	CCC	154
Tyr	Arg	Glu	Val	Leu	Pro	Leu	Ala	Thr	Phe	Val	Arg	Arg	Leu	Gly	Pro	
			20				25						30			

CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT TTC CGC GCG Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala 35 40 45	202
CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC GCA CGG CCG CCC Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro Pro 50 55 60 65	250
CCC GCC CCC TCC TTC CGC CAG GTG TCC TGC CTG AAG GAG CTG GTG Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu Val 70 75 80	298
GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC GGC GCG AAG AAC GTG CTG Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu 85 90 95	346
GCC TTC GGC TTC GCG CTG CTG GAC GGG GCC CGC GGG GGC CCC CCC GAG Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu 100 105 110	394
GCC TTC ACC ACC AGC GTG CGC AGC TAC CTG CCC AAC ACG GTG ACC GAC Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp 115 120 125	442
GCA CTG CGG GGG AGC GGG GCG TGG GGG CTG CTG CGC CGC GTG GGC Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly 130 135 140 145	490
GAC GAC GTG CTG GTT CAC CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu 150 155 160	538
GTG GCT CCC AGC TGC GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln 165 170 175	586
CTC GGC GCT GCC ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro 180 185 190	634
CGA AGG CGT CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu 195 200 205	682
GCC GGG GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly 210 215 220 225	730
GGC AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly 230 235 240	778
GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG GCC Ala Ala Pro Glu Pro Leu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala 245 250 255	826
CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT GTG GTG His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val 260 265 270	874

TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG GGT GCG CTC Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu 275 280 285	922
TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC CAG CAC CAC GCG Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala 290 295 300 305	970
GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC TGG GAC ACG CCT TGT Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys 310 315 320	1018
CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC CTC TAC TCC TCA GGC GAC Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp 325 330 335	1066
AAG GAG CAG CTG CGG CCC TCC TTC CTA CTC AGC TCT CTG AGG CCC AGC Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser 340 345 350	1114
CTG ACT GGC GCT CGG AGG CTC GTG GAG ACC ATC TTT CTG GGT TCC AGG Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg 355 360 365	1162
CCC TGG ATG CCA GGG ACT CCC CGC AGG TTG CCC CGC CTG CCC CAG CGC Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg 370 375 380 385	1210
TAC TGG CAA ATG CGG CCC CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala 390 395 400	1258
CAG TGC CCC TAC GGG GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala 405 410 415	1306
GCG GTC ACC CCA GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly 420 425 430	1354
TCT GTG GCG GCC CCC GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG Ser Val Ala Ala Pro Glu Glu Asp Thr Asp Pro Arg Arg Leu Val 435 440 445	1402
CAG CTG CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val 450 455 460 465	1450
CGG GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg 470 475 480	1498
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC CTG His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu 485 490 495	1546
GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG ATG AGC Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser 500 505 510	1594

GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT GGC TGT GTT		1642
Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val		
515 520 525		
CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG GCC AAG TTC CTG		1690
Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu		
530 535 540 545		
CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG CTC AGG TCT TTC TTT		1738
His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe		
550 555 560		
TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC AGG CTC TTT TTC TAC CGG		1786
Tyr Val Thr Glu Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg		
565 570 575		
CCG AGT GTC TGG AGC AAG TTG CAA AGC ATT GGA ATC AGA CAG CAC TTG		1834
Pro Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu		
580 585 590		
AAG AGG GTG CAG CTG CGG GAG CTG TCG GAA GCA GAG GTC AGG CAG CAT		1882
Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His		
595 600 605		
CGG GAA GCC AGG CCC GCC CTG CTG ACG TCC AGA CTC CGC TTC ATC CCC		1930
Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro		
610 615 620 625		
AAG CCT GAC GGG CTG CGG CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA		1978
Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly		
630 635 640		
GCC AGA ACG TTC CGC AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG		2026
Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg		
645 650 655		
GTG AAG GCA CTG TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC		2074
Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro		
660 665 670		
GGC CTC CTG GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC		2122
Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala		
675 680 685		
TGG CGC ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG		2170
Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu		
690 695 700 705		
CTG TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC		2218
Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro		
710 715 720		
CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG AAC		2266
Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn		
725 730 735		
ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC CAT GGG		2314
Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly		
740 745 750		

CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC TCT ACC TTG ACA GAC CTC His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu 755 760 765	2362
CAG CCG TAC ATG CGA CAG TTC GTG GCT CAC CTG CAG GAG ACC AGC CCG Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro 770 775 780 785	2410
CTG AGG GAT GCC GTC GTC ATC GAG CAG AGC TCC TCC CTG AAT GAG GCC Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Leu Asn Glu Ala 790 795 800	2458
AGC AGT GGC CTC TTC GAC GTC TTC CTA CGC TTC ATG TGC CAC CAC GCC Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala 805 810 815	2506
GTG CGC ATC AGG GGC AAG TCC TAC GTC CAG TGC CAG GGG ATC CCG CAG Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln 820 825 830	2554
GGC TCC ATC CTC TCC ACG CTG CTC TGC AGC CTG TGC TAC GGC GAC ATG Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met 835 840 845	2602
GAG AAC AAG CTG TTT GCG GGG ATT CGG CGG GAC GGG CTG CTC CTG CGT Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg 850 855 860 865	2650
TTG GTG GAT GAT TTC TTG TTG GTG ACA CCT CAC CTC ACC CAC GCG AAA Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys 870 875 880	2698
ACC TTC CTC AGG ACC CTG GTC CGA GGT GTC CCT GAG TAT GGC TGC GTG Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val 885 890 895	2746
GTG AAC TTG CGG AAG ACA GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala 900 905 910	2794
CTG GGT GGC ACG GCT TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro 915 920 925	2842
TGG TGC GGC CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp 930 935 940 945	2890
TAC TCC AGC TAT GCC CGG ACC TCC ATC AGA GCC AGT GTC ACC TTC AAC Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Val Thr Phe Asn 950 955 960	2938
CGC GGC TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG GTC Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val 965 970 975	2986
TTG CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG AAC AGC Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser 980 985 990	3034

CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG CTG CAG GCG Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala 995 1000 1005	3082
TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT CAT CAG CAA GTT Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val 1010 1015 1020 1025	3130
TGG AAG AAC CCC ACA TTT TTC CTG CGC GTC ATC TCT GAC ACG GCC TCC Trp Lys Asn Pro Thr Phe Leu Arg Val Ile Ser Asp Thr Ala Ser 1030 1035 1040	3178
CTC TGC TAC TCC ATC CTG AAA GCA AAG AAC GCA GGG ATG TCG CTG GGG Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly 1045 1050 1055	3226
GCC AAG GGC GCC GCC GGC CCT CTG CCC TCC GAG GCC GTG CAG TGG CTG Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu 1060 1065 1070	3274
TGC CAC CAA GCA TTC CTG CTC AAG CTG ACT CGA CAC CGT GTC ACC TAC Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr 1075 1080 1085	3322
G TG CCA CTC CTG GGG TCA CTC AGG ACA GCC CAG ACG CAG CTG AGT CGG Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg 1090 1095 1100 1105	3370
AAG CTC CCG GGG ACG ACG CTG ACT GCC CTG GAG GCC GCA GCC AAC CCG Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro 1110 1115 1120	3418
GCA CTG CCC TCA GAC TTC AAG ACC ATC CTG GAC TGATGGCCAC CCGCCCACAG Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp 1125 1130	3471
CCAGGCCGAG AGCAGACACC AGCAGCCCTG TCACGCCGGG CTCTACGTCC CAGGGAGGGA	3531
GGGGCGGCCACACACCCAGGC CCGCACCGCT GGGAGTCTGA GGCCTGAGTG AGTGTGTTGGC	3591
CGAGGCCCTGC ATGTCCGGCT GAAGGCTGAG TGTCCGGCTG AGGCCTGAGC GAGTGTCCAG	3651
CCAAGGGCTG AGTGTCCAGC ACACCTGCCG TCTTCACTTC CCCACAGGCT GGCGCTCGGC	3711
TCCACCCAG GGCCAGCTTT TCYTCACCAAG GAGCCCGGCT TCCACTCCCC ACATAGGAAT	3771
AGTCCATCCC CAGATTGCC ATTGTTCACCC CYTCGCCCTG CCYTCCTTTG CCTTCCACCC	3831
CCACCATCCA GGTGGAGACC CTGAGAAGGA CCCTGGGAGC TCTGGGAATT TGGAGTGACC	3891
AAAGGTGTGC CCTGTACACA GGCGAGGACC CTGCACCTGG ATGGGGTCC CTGTGGGTCA	3951
AATTGGGGGG AGGTGCTGTG GGAGTAAAAT ACTGAATATA TGAGTTTTTC AGTTTGRAA	4011
AAAAAAAAAA AAAAAAAAAA AAAAAAA	4038

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1132 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Pro Pro
100 105 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg Arg Val
130 135 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
145 150 155 160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
180 185 190

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
195 200 205

Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
210 215 220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
225 230 235 240

Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
245 250 255

Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
260 265 270

Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560
 Phe Tyr Val Thr Glu Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575
 Arg Pro Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590

Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605

His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620

Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640

Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655

Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670

Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685

Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700

Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720

Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
 725 730 735

Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
 740 745 750

Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
 755 760 765

Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
 770 775 780

Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
 785 790 795 800

Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
 805 810 815

Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
 820 825 830

Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
 835 840 845

Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
 850 855 860

Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
 865 870 875 880

Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
 885 890 895

Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
 900 905 910

Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
 915 920 925
 Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
 930 935 940
 Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Val Thr Phe
 945 950 955 960
 Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
 965 970 975
 Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
 980 985 990
 Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Gln
 995 1000 1005
 Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
 1010 1015 1020
 Val Trp Lys Asn Pro Thr Phe Leu Arg Val Ile Ser Asp Thr Ala
 1025 1030 1035 1040
 Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu
 1045 1050 1055
 Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp
 1060 1065 1070
 Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr
 1075 1080 1085
 Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser
 1090 1095 1100
 Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn
 1105 1110 1115 1120
 Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 1125 1130

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Trp Xaa Phe Phe Tyr
 1 5 10 15
 Xaa Thr Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa
 20 25 30

Xaa Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile
35 40

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Trp Xaa Phe Phe Tyr
1 5 10 15

Xaa Thr Glu Xaa Arg Xaa
20 25 30

Xaa Xaa Trp Xaa Xaa Xaa Xaa Xaa Xaa Ile
35 40

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Glu Xaa Xaa Val Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3855 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 56..2479
(D) OTHER INFORMATION: /product= "hTRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GCAGCGCTGC	GTCCTGCTGC	GCACGTGGGA	AGCCCTGGCC	CCGGCCACCC	CCGCG	ATG	58									
						Met										
						1										
CCG	CGC	GCT	CCC	CGC	TGC	CGA	GCC	GTG	CGC	TCC	CTG	CTG	CGC	AGC	CAC	106
Pro	Arg	Ala	Pro	Arg	Cys	Arg	Ala	Val	Arg	Ser	Leu	Leu	Arg	Ser	His	
5								10					15			
TAC	CGC	GAG	GTG	CTG	CCG	CTG	GCC	ACG	TTC	GTG	CGG	CGC	CTG	GGG	CCC	154
Tyr	Arg	Glu	Val	Leu	Pro	Leu	Ala	Thr	Phe	Val	Arg	Arg	Leu	Gly	Pro	
20								25					30			
CAG	GGC	TGG	CGG	CTG	GTG	CAG	CGC	GGG	GAC	CCG	GCG	GCT	TTC	CGC	GCG	202
Gln	Gly	Trp	Arg	Leu	Val	Gln	Arg	Gly	Asp	Pro	Ala	Ala	Phe	Arg	Ala	
35						40					45					
CTG	GTG	GCC	CAG	TGC	CTG	GTG	TGC	GTG	CCC	TGG	GAC	GCA	CGG	CCG	CCC	250
Leu	Val	Ala	Gln	Cys	Leu	Val	Cys	Val	Pro	Trp	Asp	Ala	Arg	Pro	Pro	
50						55			60			65				
CCC	GCC	GCC	CCC	TCC	TTC	CGC	CAG	GTG	TCC	TGC	CTG	AAG	GAG	CTG	GTG	298
Pro	Ala	Ala	Pro	Ser	Phe	Arg	Gln	Val	Ser	Cys	Leu	Lys	Glu	Leu	Val	
70						75					80					
GCC	CGA	GTG	CTG	CAG	AGG	CTG	TGC	GAG	CGC	GGC	GCG	AAG	AAC	GTG	CTG	346
Ala	Arg	Val	Leu	Gln	Arg	Leu	Cys	Glu	Arg	Gly	Ala	Lys	Asn	Val	Leu	
85						90					95					
GCC	TTC	GGC	TTC	GCG	CTG	CTG	GAC	GGG	GCC	CGC	GGG	GGC	CCC	CCC	GAG	394
Ala	Phe	Gly	Phe	Ala	Leu	Leu	Asp	Gly	Ala	Arg	Gly	Gly	Pro	Pro	Glu	
100						105					110					
GCC	TTC	ACC	ACC	AGC	GTG	CGC	AGC	TAC	CTG	CCC	AAC	ACG	GTG	ACC	GAC	442
Ala	Phe	Thr	Thr	Ser	Val	Arg	Ser	Tyr	Leu	Pro	Asn	Thr	Val	Thr	Asp	
115						120			125							
GCA	CTG	CGG	GGG	AGC	GGG	GCG	TGG	GGG	CTG	CTG	CTG	CGC	CGC	GTG	GGC	490
Ala	Leu	Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Leu	Arg	Arg	Val	Gly	
130						135			140			145				
GAC	GAC	GTG	CTG	GTT	CAC	CTG	GCA	CGC	TGC	GCG	CTC	TTT	GTG	CTG	538	
Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu	Phe	Val	Leu	
150						155					160					
GTG	GCT	CCC	AGC	TGC	GCC	TAC	CAG	GTG	TGC	GGG	CCG	CCG	CTG	TAC	CAG	586
Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro	Leu	Tyr	Gln	
165						170					175					
CTC	GGC	GCT	GCC	ACT	CAG	GCC	CGG	CCC	CCG	CCA	CAC	GCT	AGT	GGA	CCC	634
Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala	Ser	Gly	Pro	
180						185					190					
CGA	AGG	CGT	CTG	GGA	TGC	GAA	CGG	GCC	TGG	AAC	CAT	AGC	GTC	AGG	GAG	682
Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser	Val	Arg	Glu	
195						200					205					
GCC	GGG	GTC	CCC	CTG	GGC	CTG	CCA	GCC	CCG	GGT	GCG	AGG	AGG	CGC	GGG	730
Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg	Arg	Arg	Gly	
210						215					220			225		

GGC AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly 230 235 240	778
GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG GCC Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala 245 250 255	826
CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT GTG GTG His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val 260 265 270	874
TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG GGT GCG CTC Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu 275 280 285	922
TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC CAG CAC CAC GCG Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala 290 295 300 305	970
GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC TGG GAC ACG CCT TGT Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys 310 315 320	1018
CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC CTC TAC TCC TCA GGC GAC Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp 325 330 335	1066
AAG GAG CAG CTG CGG CCC TCC TTC CTA CTC AGC TCT CTG AGG CCC AGC Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser 340 345 350	1114
CTG ACT GGC GCT CGG AGG CTC GTG GAG ACC ATC TTT CTG GGT TCC AGG Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg 355 360 365	1162
CCC TGG ATG CCA GGG ACT CCC CGC AGG TTG CCC CGC CTG CCC CAG CGC Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg 370 375 380 385	1210
TAC TGG CAA ATG CGG CCC CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala 390 395 400	1258
CAG TGC CCC TAC GGG GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala 405 410 415	1306
GCG GTC ACC CCA GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly 420 425 430	1354
TCT GTG GCG GCC CCC GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val 435 440 445	1402
CAG CTG CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val 450 455 460 465	1450

CGG GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg 470	475	480	1498
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC CTG His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu 485	490	495	1546
GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG ATG AGC Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser 500	505	510	1594
GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT GGC TGT GTT Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val 515	520	525	1642
CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG GCC AAG TTC CTG Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu 530	535	540	1690
CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG CTC AGG TCT TTC TTT His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe 550	555	560	1738
TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC AGG CTC TTT TTC TAC CGG Tyr Val Thr Glu Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg 565	570	575	1786
AAG AGT GTC TGG AGC AAG TTG CAA AGC ATT GGA ATC AGA CAG CAC TTG Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu 580	585	590	1834
AAG AGG GTG CAG CTG CGG GAG CTG TCG GAA GCA GAG GTC AGG CAG CAT Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His 595	600	605	1882
CGG GAA GCC AGG CCC GCC CTG CTG ACG TCC AGA CTC CGC TTC ATC CCC Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro 610	615	620	1930
AAG CCT GAC GGG CTG CGG CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly 630	635	640	1978
GCC AGA ACG TTC CGC AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg 645	650	655	2026
GTG AAG GCA CTG TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro 660	665	670	2074
GCG CTC CTG GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala 675	680	685	2122
TGG CGC ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu 690	695	700	2170
		705	

CTG TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro 710 715 720	2218
CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG AAC Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn 725 730 735	2266
ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC CAT GGG Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly 740 745 750	2314
CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC CTA CGT CCA GTG CCA GGG His Val Arg Lys Ala Phe Lys Ser His Val Leu Arg Pro Val Pro Gly 755 760 765	2362
GAT CCC GCA GGG CTC CAT CCT CTC CAC GCT GCT CTG CAG CCT GTG CTA Asp Pro Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val Leu 770 775 780 785	2410
CGG CGA CAT GGA GAA CAA GCT GTT TGC GGG GAT TCG GCG GGA CGG GCT Arg Arg His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg Ala 790 795 800	2458
GCT CCT GCG TTT GGT GGA TGATTCTTG TTGGTGACAC CTCACCTCAC Ala Pro Ala Phe Gly Gly 805	2506
CCACCGGAAA ACCTTCCTCA GGACCCCTGGT CCGAGGTGTC CCTGAGTATG GCTGCGTGGT	2566
GAACATTGCGG AAGACAGTGG TGAACCTCCC TGTAGAACGAC GAGGCCCTGG GTGGCACGGC	2626
TTTGTTTCAG ATGCCGGCCC ACGGCCTATT CCCCTGGTGC GGCCTGCTGC TGGATACCCG	2686
GACCCCTGGAG GTGCAGAGCG ACTACTCCAG CTATGCCCG ACCTCCATCA GAGCCAGTCT	2746
CACCTTCAAC CGCGGCTTCA AGGCTGGAG GAACATGCGT CGCAAACCTCT TTGGGGTCTT	2806
GC GGCTGAAG TGTACAGGCC TGTTCCTGGA TTTGCAGGTG AACAGCCTCC AGACGGTGTG	2866
CACCAACATC TACAAGATCC TCCTGCTGCA GGCGTACAGG TTTCACGCAT GTGTGCTGCA	2926
GCTCCCATT CATCAGCAAG TTTGGAAGAA CCCCACATT TTCCTGCGCG TCATCTCTGA	2986
CACGGCCTCC CTCTGCTACT CCATCCTGAA AGCCAAGAAC GCAGGGATGT CGCTGGGGC	3046
CAAGGGCGCC GCCGGCCCTC TGCCCTCCGA GGCGTGCAG TGGCTGTGCC ACCAAGCATT	3106
CCTGCTCAAG CTGACTCGAC ACCGTGTCAC CTACGTGCCA CTCCTGGGT CACTCAGGAC	3166
AGCCCAGACG CAGCTGAGTC GGAAGCTCCC GGGGACGACG CTGACTGCC TGGAGGCCGC	3226
AGCCAACCCG GCACTGCCCT CAGACTTCAA GACCATCCTG GACTGATGGC CACCCGCCA	3286
CAGCCAGGCC GAGAGCAGAC ACCAGCAGCC CTGTCACGCC GGGCTCTACG TCCCAGGGAG	3346
GGAGGGCGGG CCCACACCCA GGCCCGCACC GCTGGGAGTC TGAGGCCTGA GTGAGTGT	3406
GGCCGAGGCC TGCATGTCCG GCTGAAGGCT GAGTGTCCGG CTGAGGCCTG AGCGAGTGT	3466
CAGCCAAGGG CTGAGTGTCC AGCACACCTG CCGTCTTCAC TTCCCCACAG GCTGGCGCTC	3526

GGCTCCACCC CAGGGCCAGC TTTTCCTCAC CAGGAGCCCG GCTTCCACTC CCCACATAGG	3586
AATAGTCCAT CCCCAGATTG GCCATTGTTG ACCCCTCGCC CTGCCCTCCT TTGCCTTCCA	3646
CCCCCACCAT CCAGGTGGAG ACCCTGAGAA GGACCCCTGGG AGCTCTGGGA ATTTGGAGTG	3706
ACCAAAGGTG TGCCCTGTAC ACAGGCGAGG ACCCTGCACC TGGATGGGGG TCCCTGTGGG	3766
TCAAATTGGG GGGAGGTGCT GTGGGAGTAA AATACTGAAT ATATGAGTTT TTCAGTTTG	3826
AAAAAAAAAA AAAAAAAAAA AAAAAAAA	3855

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 807 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser			
1	5	10	15
His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly			
20	25	30	
Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg			
35	40	45	
Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro			
50	55	60	
Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu			
65	70	75	80
Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val			
85	90	95	
Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro			
100	105	110	
Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr			
115	120	125	
Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg Arg Val			
130	135	140	
Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val			
145	150	155	160
Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr			
165	170	175	
Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly			
180	185	190	

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
 195 200 205
 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
 210 215 220
 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
 225 230 235 240
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
 245 250 255
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430
 Gly Ser Val Ala Ala Pro Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510

Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590
 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720
 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
 725 730 735
 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
 740 745 750
 Gly His Val Arg Lys Ala Phe Lys Ser His Val Leu Arg Pro Val Pro
 755 760 765
 Gly Asp Pro Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val
 770 775 780
 Leu Arg Arg His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg
 785 790 795 800
 Ala Ala Pro Ala Phe Gly Gly
 805

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3025 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..3025
- (D) OTHER INFORMATION: /note= "mouse TRT cDNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

CGGGTGGGAG	GCCCATCCCG	GCCTTGAGCA	CAATGACCCG	CGCTCCTCGT	TGCCCCGCGG	60
TGCGCTCTCT	GCTGCGCAGC	CGATACCGGG	AGGTGTGGCC	GCTGGCAACC	TTTGTGCGGC	120
GCCTGGGGCC	CGAGGGCAGG	CGGCTTGTGC	AACCCGGGGA	CCCGAAGATC	TACCGCACTT	180
TGGTTGCCCA	ATGCCTAGTG	TGCATGCACT	GGGGCTCACA	GCCTCCACCT	GCCGACCTTT	240
CCTTCCACCA	GGTGTCACTCC	CTGAAAGAGC	TGGTGGCCAG	GGTTGTGCAG	AGACTCTGCG	300
AGCGCAACGA	GAGAAACGTG	CTGGCTTTG	GCTTGAGCT	GCTTAACGAG	GCCAGAGGCG	360
GGCCTCCCAT	GGCCTTCACT	AGTAGCGTGC	GTAGCTACTT	GCCCAACACT	GTTATTGAGA	420
CCCTGCGTGT	CAGGGTGCA	TGGATGCTAC	TGTTGAGCCG	AGTGGCGAC	GACCTGCTGG	480
TCTACCTGCT	GGCACACTGT	GCTCTTATC	TTCTGGTGCC	CCCCAGCTGT	GCCTACCAGG	540
TGTGTGGGTC	TCCCCGTAC	CAAATTGTG	CCACCAACGGA	TATCTGGCCC	TCTGTGTCCG	600
CTAGTTACAG	GCCCACCCGA	CCCGTGGCA	GGAATTCAC	TAACCTTAGG	TTCTTACAAC	660
AGATCAAGAG	CAGTAGTCGC	CAGGAAGCAC	CGAAACCCCT	GGCCTTGCCA	TCTCGAGGTA	720
CAAAGAGGCA	TCTGAGTCTC	ACCAAGTACAA	GTGTGCCCTC	AGCTAAGAAG	GCCAGATGCT	780
ATCCTGTCCC	GAGAGTGGAG	GAGGGACCCC	ACAGGGCAGGT	GCTACCAACC	CCATCAGGCA	840
AATCATGGGT	GCCAAGTCCT	GCTCGGTCCC	CCGAGGTGCC	TACTGCAGAG	AAAGATTTGT	900
CTTCTAAAGG	AAAGGTGTCT	GACCTGAGTC	TCTCTGGGTC	GGTGTGCTGT	AAACACAAGC	960
CCAGCTCCAC	ATCTCTGCTG	TCACCACCCC	GCCAAAATGC	CTTCAGCTC	AGGCCATTAA	1020
TTGAGACCAG	ACATTCCTT	TACTCCAGGG	GAGATGGCCA	AGAGCGTCTA	AACCCCTCAT	1080
TCCTACTCAG	CAACCTCCAG	CCTAACTTGA	CTGGGGCCAG	GAGACTGGTG	GAGATCATCT	1140
TTCTGGGCTC	AAGGCCTAGG	ACATCAGGAC	CACTCTGCAG	GACACACCGT	CTATCGCGTC	1200
GATACTGGCA	GATGCGGCC	CTGTTCCAAC	AGCTGCTGGT	GAACCATGCA	GAGTGCCAAT	1260

ATGTCAGACT CCTCAGGTCA CATTGCAGGT TTGAAACAGC AAACCAACAG GTGACAGATG	1320
CCTTGAACAC CAGCCCACCG CACCTCATGG ATTGCTCCG CCTGCACAGC AGTCCCTGGC	1380
AGGTATATGG TTTCTTCGG GCCTGTCTCT GCAAGGTGGT GTCTGCTAGT CTCTGGGTA	1440
CCAGGCACAA TGAGCGCCGC TTCTTAAGA ACTTAAAGAA GTTCATCTCG TTGGGGAAAT	1500
ACGGCAAGCT ATCACTGCAG GAACTGATGT GGAAGATGAA AGTAGAGGAT TGCCACTGGC	1560
TCCGCAGCAG CCCGGGAAG GACCGTGTCC CCGCTGCAGA GCACCGTCTG AGGGAGAGGA	1620
TCCTGGCTAC GTTCTGTTC TGGCTGATGG ACACATACGT GGTACAGCTG CTTAGGTCA	1680
TCTTTACAT CACAGAGAGC ACATTCCAGA AGAACAGGCT CTTCTCTAC CGTAAGAGTG	1740
TGTGGAGCAA GCTGCAGAGC ATTGGAGTCA GGCAACACCT TGAGAGAGTG CGGCTACGGG	1800
AGCTGTCACA AGAGGAGGTC AGGCATCACC AGGACACCTG GCTAGCCATG CCCATCTGCA	1860
GAUTGCGCTT CATCCCCAAG CCCAACGGCC TGCGGCCAT TGTGAACATG AGTTATAGCA	1920
TGGGTACCAAG AGCTTTGGC AGAAGGAAGC AGGCCCAGCA TTTCACCCAG CGTCTCAAGA	1980
CTCTCTTCAG CATGCTAAC TATGAGCCGA CAAACATCC TCACCTTATG GGGTCTTCTG	2040
TACTGGGTAT GAATGACATC TACAGGACCT GGCGGCCTT TGTGCTGCGT GTGCGTGCTC	2100
TGGACCANAC ACCANGATGT ACTTTGTTAA GGCAGATGTG ACCGGGCCT ATGATGCCAT	2160
CCCCAGGGTA AGCTGGGTGN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	2220
TGGTGGAGGT TGTTGCCAAT ATGATCAGGC ATTGGAGAG CACGTACTGT ATCCGCCAGT	2280
ATGCAGTGGT CCGGAGAGAT AGCCAAGGCC AAGTCCACAA GTCNTTCTAG AGACAGGTCA	2340
CCACCTTCTC TGACTTCCAG CCATACATGG GCCAGTTCCCT TAAGCATCTG CAGGATTCA	2400
ATGCCAGTGC ACTGAGGAAC TCCGTTGTCA TCGAGCAGAG CATCTCTATG AATGAGAGCA	2460
GCAGCAGCCT GTTGATTCT TCCTGCACCT CCTGCGTCAC AGTGTGTA AGATTGGTGA	2520
CAGGTGCTAT ACGCAGTGCC AGGGCATCCC CCAGGGCTCC AGCCTATCCA CCCTGCTCTG	2580
CAGTCTGTGT TTCGGAGACA TGGAGAACAA GCTGTTGCT GAGGTGCAGC GGGATGGGTT	2640
GCTTTACGT TTTGTTGATG ACTTTCTGTT GGTGACGCCT CACTGGACC AAGCANNNN	2700
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	2760
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	2820
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	2880
NNNNNNNNNN CTGCAGTTAT GCCCAGACCT CAATTAAGAC GAGCCTCACC TTCCAGAGTG	2940
TCTTCAAAGC TGGGAAGACC ATGCGGAACA AGCTCCTGTC GGTCTTGCAG TTGAAGTGTC	3000
ACGGTCTATT TCTAGACTTG CAGGT	3025

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

CTTTTACATC ACAGAGAGCA C

21

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

CTCGGACCAAG GGTCTGAGG AA

22

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Cys	Gly	Gly	Gln	Lys	Gln	Leu	Glu	Phe	Tyr	Phe	Ser	Asp	Ala	Asn	Leu
1				5					10					15	
Tyr	Asn	Asp	Ser	Phe	Leu										
				20											

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Asn Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn Asn
1 5 10 15
Glu Phe Arg Ile Ile
20

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Cys Leu Pro Glu Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr
1 5 10 15
Asp Ser Ile Pro Arg Met Glu Cys Met Arg Ile Leu Lys
20 25

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1285 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Met Ser Asp Lys Ile Ile His Leu Thr Asp Asp Ser Phe Asp Thr Asp
1 5 10 15
Val Leu Lys Ala Asp Gly Ala Ile Leu Val Asp Phe Trp Ala His Trp
20 25 30
Cys Gly Pro Cys Lys Met Ile Ala Pro Ile Leu Asp Glu Ile Ala Asp
35 40 45
Glu Tyr Gln Gly Lys Leu Thr Val Ala Lys Leu Arg Ile Asp His Asn
50 55 60
Pro Gly Thr Ala Pro Lys Tyr Gly Ile Arg Gly Ile Pro Thr Leu Leu
65 70 75 80
Leu Phe Lys Asn Gly Glu Val Ala Ala Thr Lys Val Gly Ala Leu Ser
85 90 95

Lys Gly Gln Leu Lys Glu Phe Leu Asp Ala Asn Leu Ala Gly Ser Gly
 100 105 110
 Ser Gly Asp Asp Asp Asp Lys Val Pro Met His Glu Leu Glu Ile Phe
 115 120 125
 Glu Phe Ala Ala Ala Ser Thr Gln Arg Cys Val Leu Leu Arg Thr Trp
 130 135 140
 Glu Ala Leu Ala Pro Ala Thr Pro Ala Met Pro Arg Ala Pro Arg Cys
 145 150 155 160
 Arg Ala Val Arg Ser Leu Leu Arg Ser His Tyr Arg Glu Val Leu Pro
 165 170 175
 Leu Ala Thr Phe Val Arg Arg Leu Gly Pro Gln Gly Trp Arg Leu Val
 180 185 190
 Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala Leu Val Ala Gln Cys Leu
 195 200 205
 Val Cys Val Pro Trp Asp Ala Arg Pro Pro Pro Ala Ala Pro Ser Phe
 210 215 220
 Arg Gln Val Ser Cys Leu Lys Glu Leu Val Ala Arg Val Leu Gln Arg
 225 230 235 240
 Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe Gly Phe Ala Leu
 245 250 255
 Leu Asp Gly Ala Arg Gly Pro Pro Glu Ala Phe Thr Thr Ser Val
 260 265 270
 Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu Arg Gly Ser Gly
 275 280 285
 Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp Val Leu Val His
 290 295 300
 Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala Pro Ser Cys Ala
 305 310 315 320
 Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly Ala Ala Thr Gln
 325 330 335
 Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg Arg Leu Gly Cys
 340 345 350
 Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly Val Pro Leu Gly
 355 360 365
 Leu Pro Ala Pro Gly Ala Arg Arg Gly Gly Ser Ala Ser Arg Ser
 370 375 380
 Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala Pro Glu Pro Glu
 385 390 395 400
 Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro Gly Arg Thr Arg
 405 410 415

Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro Ala Arg Pro Ala
 420 425 430

Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly Thr Arg His Ser
 435 440 445

His Pro Ser Val Gly Arg Gln His His Ala Gly Pro Pro Ser Thr Ser
 450 455 460

Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu
 465 470 475 480

Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro
 485 490 495

Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg
 500 505 510

Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp Met Pro Gly Thr
 515 520 525

Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp Gln Met Arg Pro
 530 535 540

Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys Pro Tyr Gly Val
 545 550 555 560

Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val Thr Pro Ala Ala
 565 570 575

Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val Ala Ala Pro Glu
 580 585 590

Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu Leu Arg Gln His
 595 600 605

Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg
 610 615 620

Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn Glu Arg Arg Phe
 625 630 635 640

Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys His Ala Lys Leu
 645 650 655

Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg Asp Cys Ala Trp
 660 665 670

Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala Ala Glu His Arg
 675 680 685

Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp Leu Met Ser Val
 690 695 700

Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr
 705 710 715 720

Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys
 725 730 735

Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg
 740 745 750

Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu Ala Arg Pro Ala
 755 760 765

Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg
 770 775 780

Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg
 785 790 795 800

Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys Ala Leu Phe Ser
 805 810 815

Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser
 820 825 830

Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu
 835 840 845

Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr Phe Val Lys Val
 850 855 860

Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu
 865 870 875 880

Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg
 885 890 895

Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe
 900 905 910

Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln
 915 920 925

Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val
 930 935 940

Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp
 945 950 955 960

Val Phe Leu Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys
 965 970 975

Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr
 980 985 990

Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala
 995 1000 1005

Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu
 1010 1015 1020

Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu
 1025 1030 1035 1040

Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr
 1045 1050 1055

Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe
 1060 1065 1070
 Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu
 1075 1080 1085
 Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg
 1090 1095 1100
 Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly
 1105 1110 1115 1120
 Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His
 1125 1130 1135
 Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr
 1140 1145 1150
 Asn Ile Tyr Lys Ile Leu Leu Gln Ala Tyr Arg Phe His Ala Cys
 1155 1160 1165
 Val Leu Gln Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe
 1170 1175 1180
 Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu
 1185 1190 1195 1200
 Lys Ala Lys Asn Ala Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly
 1205 1210 1215
 Pro Leu Pro Ser Glu Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu
 1220 1225 1230
 Leu Lys Leu Thr Arg His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser
 1235 1240 1245
 Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr
 1250 1255 1260
 Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe
 1265 1270 1275 1280
 Lys Thr Ile Leu Asp
 1285

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 538 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205

Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220

Gly Ser Arg Arg Ala Ser Val Gly Ser Val Thr Lys Ile Pro Gln Gly
 225 230 235 240

Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu
 245 250 255

Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu
 260 265 270

Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys Thr
 275 280 285

Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val
 290 295 300

Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu
 305 310 315 320

Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro Trp
 325 330 335

Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr
 340 345 350
 Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Val Thr Phe Asn Arg
 355 360 365
 Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu
 370 375 380
 Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu
 385 390 395 400
 Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Gln Ala Tyr
 405 410 415
 Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val Trp
 420 425 430
 Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu
 435 440 445
 Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly Ala
 450 455 460
 Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu Cys
 465 470 475 480
 His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr Val
 485 490 495
 Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg Lys
 500 505 510
 Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro Ala
 515 520 525
 Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 530 535

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205

Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220

Gly Ser Arg Arg Ala Ser Val Gly Ser Val His His His His His His
 225 230 235 240

His His Gly Ser Val Thr Lys Met Ser Val Tyr Val Val Glu Leu Leu
 245 250 255

Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu
 260 265 270

Phe Phe Tyr Arg Pro Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile
 275 280 285

Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu
 290 295 300

Val Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu
 305 310 315 320

Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp
 325 330 335

Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg
 340 345 350

Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg
 355 360 365

Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp
 370 375 380
 Ile His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp
 385 390 395 400
 Pro Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr
 405 410 415
 Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile
 420 425 430
 Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys
 435 440 445
 Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr
 450 455 460
 Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln
 465 470 475 480
 Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser
 485 490 495
 Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met
 500 505 510
 Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln
 515 520 525
 Gly Ile
 530

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80

Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu
					85				90					95	
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser
					100				105				110		
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu
					115			120				125			
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn
					130			135			140				
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp
					145			150			155			160	
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu
					165				170				175		
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr
					180				185			190			
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala
					195				200			205			
Thr	Phe	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg	
					210			215			220				
Gly	Ser	Arg	Arg	Ala	Ser	Val	Gly	Ser	Val	Thr	Lys	Met	Ser	Val	Tyr
					225			230			235			240	
Val	Val	Glu	Leu	Leu	Arg	Ser	Phe	Phe	Tyr	Val	Thr	Glu	Thr	Thr	Phe
					245				250				255		
Gln	Lys	Asn	Arg	Leu	Phe	Phe	Tyr	Arg	Pro	Ser	Val	Trp	Ser	Lys	Leu
					260				265			270			
Gln	Ser	Ile	Gly	Ile	Arg	Gln	His	Leu	Lys	Arg	Val	Gln	Leu	Arg	Glu
					275				280			285			
Leu	Ser	Glu	Ala	Glu	Val	Arg	Gln	His	Arg	Glu	Ala	Arg	Pro	Ala	Leu
					290			295			300				
Leu	Thr	Ser	Arg	Leu	Arg	Phe	Ile	Pro	Lys	Pro	Asp	Gly	Leu	Arg	Pro
					305			310			315			320	
Ile	Val	Asn	Met	Asp	Tyr	Val	Val	Gly	Ala	Arg	Thr	Phe	Arg	Arg	Glu
					325				330			335			
Lys	Arg	Ala	Glu	Arg	Leu	Thr	Ser	Arg	Lys	Ala	Leu	Phe	Ser	Val	Leu
					340				345			350			
Asn	Tyr	Glu	Arg	Ala	Arg	Arg	Pro	Gly	Leu	Leu	Gly	Ala	Ser	Val	Leu
					355				360			365			
Gly	Leu	Asp	Asp	Ile	His	Arg	Ala	Trp	Arg	Thr	Phe	Val	Leu	Arg	Val
					370			375			380				
Arg	Ala	Gln	Asp	Pro	Pro	Pro	Glu	Tyr	Phe	Val	Lys	Val	Asp	Val	Thr
					385			390			395			400	

Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala
 405 410 415
 Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val
 420 425 430
 Val Gln Lys Ala Ala His Gly Val Arg Lys Ala Phe Lys Ser His Val
 435 440 445
 Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His
 450 455 460
 Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser
 465 470 475 480
 Ser Ser Leu Asn Glu Ala Ser Gly Leu Phe Asp Val Phe Leu Arg Phe
 485 490 495
 Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys
 500 505 510
 Gln Gly Ile
 515

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205

Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220

Gly Ser Arg Arg Ala Ser Val Gly Ser Val Thr Lys Ala Thr Ser Leu
 225 230 235 240

Glu Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg
 245 250 255

Gln His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp
 260 265 270

Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr
 275 280 285

Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser
 290 295 300

Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe
 305 310 315 320

Leu Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg
 325 330 335

Leu Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu
 340 345 350

Gly Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys
 355 360 365

Pro Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu
 370 375 380

Lys Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Asp Thr Asp Pro
 385 390 395 400

Arg Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val
 405 410 415

Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu
 420 425 430

Trp Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys
 435 440 445

Phe Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr
 450 455 460
 Trp Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly
 465 470 475 480
 Val Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu
 485 490 495
 Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu
 500 505 510
 Arg Ser

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 517 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Arg Arg Ala Ser Val Gly Ser Val Thr Lys Met Pro Arg Ala
 225 230 235 240
 Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Ser His Tyr Arg Glu Val
 245 250 255
 Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly Pro Gln Gly Trp Arg
 260 265 270
 Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala Leu Val Ala Gln
 275 280 285
 Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro Pro Ala Ala Pro Ser
 290 295 300
 Phe Arg Gln Val Ser Cys Leu Lys Glu Leu Val Ala Arg Val Leu Gln
 305 310 315 320
 Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe Gly Phe Ala
 325 330 335
 Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Thr Thr Ser Val
 340 345 350
 Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu Arg Gly Ser Gly
 355 360 365
 Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp Val Leu Val His
 370 375 380
 Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala Pro Cys Ala Tyr
 385 390 395 400
 Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala
 405 410 415
 Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu
 420 425 430
 Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly Val Pro Leu Gly Leu
 435 440 445
 Pro Ala Pro Gly Ala Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu
 450 455 460
 Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg
 465 470 475 480
 Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro Gly Arg Thr Arg Gly
 485 490 495

Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro Ala Arg Pro Ala Glu
500 505 510
Glu Ala Thr Ser Leu
515

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

CCGGCCACCC CCCATATGCC GCGCGCTCCC 30

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

TGCGCACGTG GGAAGCCCTG GCAGATCTGA ATTCCACCAT GCCGCGCGCT CCCCCGCTG 58

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

CGGGACGGGC TGCTCCTGCG TTTGGTGGAC GCGTTCTTGT TGGTGACACC TCACCTCAC 60

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

Xaa Xaa Xaa Arg Xaa Xaa Pro Lys Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
100 105 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
130 135 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
145 150 155 160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
 165 170 175
 Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
 180 185 190
 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
 195 200 205
 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
 210 215 220
 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
 225 230 235 240
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
 245 250 255
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480

Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560
 Phe Tyr Val Thr Glu Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590
 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720
 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
 725 730 735
 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
 740 745 750
 Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
 755 760 765
 Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
 770 775 780
 Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
 785 790 795 800

Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
 805 810 815
 Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
 820 825 830
 Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
 835 840 845
 Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
 850 855 860
 Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
 865 870 875 880
 Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
 885 890 895
 Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
 900 905 910
 Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
 915 920 925
 Pro Trp Cys Gly Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
 930 935 940
 Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe
 945 950 955 960
 Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
 965 970 975
 Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
 980 985 990
 Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Gln
 995 1000 1005
 Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
 1010 1015 1020
 Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala
 1025 1030 1035 1040
 Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu
 1045 1050 1055
 Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp
 1060 1065 1070
 Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr
 1075 1080 1085
 Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser
 1090 1095 1100
 Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Asn
 1105 1110 1115 1120

Pro	Ala	Leu	Pro	Ser	Asp	Phe	Lys	Thr	Ile	Leu	Asp	Leu	Glu	Gln	Lys	
														1125	1130	1135

Leu	Ile	Ser	Glu	Glu	Asp	Leu	Asn	Ser	Ala	Val	Asp	His	His	His	His		
															1140	1145	1150

His	His																
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(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Met	Pro	Arg	Gly	Ser	His	His	His	His	His	Gly	Met	Ala	Ser	Met
1														15

Thr	Gly	Gly	Gln	Gln	Met	Gly	Arg	Asp	Leu	Tyr	Asp	Asp	Asp	Asp	Leu
														30	

20														
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Asp	Pro	Ser	Ser	Arg	Ser	Ala	Ala	Gly	Thr	Met	Glu	Phe	Ala	Ala	Ala
35														45	

Ser	Thr	Gln	Arg	Cys	Val	Leu	Leu	Arg	Thr	Trp	Glu	Ala	Leu	Ala	Pro
50														60	

Ala	Thr	Pro	Ala	Met	Pro	Arg	Ala	Pro	Arg	Cys	Arg	Ala	Val	Arg	Ser
65														80	

Leu	Leu	Arg	Ser	His	Tyr	Arg	Glu	Val	Leu	Pro	Leu	Ala	Thr	Phe	Val
85														95	

Arg	Arg	Leu	Gly	Pro	Gln	Gly	Trp	Arg	Leu	Val	Gln	Arg	Gly	Asp	Pro
100														110	

Ala	Ala	Phe	Arg	Ala	Leu	Val	Ala	Gln	Cys	Leu	Val	Cys	Val	Pro	Trp
115														125	

Asp	Ala	Arg	Pro	Pro	Ala	Ala	Pro	Ser	Phe	Arg	Gln	Val	Ser	Cys	
130														140	

Leu	Lys	Glu	Leu	Val	Ala	Arg	Val	Leu	Gln	Arg	Leu	Cys	Glu	Arg	Gly
145														160	

Ala	Lys	Asn	Val	Leu	Ala	Phe	Gly	Phe	Ala	Leu	Leu	Asp	Gly	Ala	Arg
165														175	

Gly	Gly	Pro	Pro	Glu	Ala	Phe	Thr	Thr	Ser	Val	Arg	Ser	Tyr	Leu	Pro
180														190	

Asn	Thr	Val	Thr	Asp	Ala	Leu	Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu
195														205	

Leu Arg Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys
 210 215 220
 Ala Leu Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly
 225 230 235 240
 Pro Pro Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro
 245 250 255
 His Ala Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn
 260 265 270
 His Ser Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly
 275 280 285
 Ala Arg Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys
 290 295 300
 Arg Pro Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly
 305 310 315 320
 Gln Gly Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg
 325 330 335
 Gly Phe Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser
 340 345 350
 Leu Glu Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly
 355 360 365
 Arg Gln His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro
 370 375 380
 Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu
 385 390 395 400
 Tyr Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser
 405 410 415
 Ser Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile
 420 425 430
 Phe Leu Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro
 435 440 445
 Arg Leu Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu
 450 455 460
 Leu Gly Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His
 465 470 475 480
 Cys Pro Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg
 485 490 495
 Glu Lys Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp
 500 505 510
 Pro Arg Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln
 515 520 525

Val Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly
 530 535 540
 Leu Trp Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys
 545 550 555 560
 Lys Phe Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu
 565 570 575
 Thr Trp Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro
 580 585 590
 Gly Val Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile
 595 600 605
 Leu Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu
 610 615 620
 Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg
 625 630 635 640
 Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly
 645 650 655
 Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala
 660 665 670
 Glu Val Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg
 675 680 685
 Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met
 690 695 700
 Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu
 705 710 715 720
 Arg Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu
 725 730 735
 Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp
 740 745 750
 Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln
 755 760 765
 Asp Pro Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala
 770 775 780
 Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile
 785 790 795 800
 Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln
 805 810 815
 Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser
 820 825 830
 Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu
 835 840 845

Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser
 850 855 860
 Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe
 865 870 875 880
 Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys
 885 890 895
 Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu
 900 905 910
 Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp
 915 920 925
 Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His
 930 935 940
 Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro
 945 950 955 960
 Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro
 965 970 975
 Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala
 980 985 990
 His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu
 995 1000 1005
 Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala
 1010 1015 1020
 Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg
 1025 1030 1035 1040
 Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp
 1045 1050 1055
 Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile
 1060 1065 1070
 Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro
 1075 1080 1085
 Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile
 1090 1095 1100
 Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala
 1105 1110 1115 1120
 Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu
 1125 1130 1135
 Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg
 1140 1145 1150
 His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln
 1155 1160 1165

Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu	1170	1175	1180
Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp	1185	1190	1195
			1200

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1189 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Met Lys Phe Leu Val Asn Val Ala Leu Val Phe Met Val Val Tyr Ile	1	5	10	15
Ser Tyr Ile Tyr Ala Asp Pro Ser Ser Arg Ser Ala Ala Gly Thr Met	20	25	30	
Glu Phe Ala Ala Ala Ser Thr Gln Arg Cys Val Leu Leu Arg Thr Trp	35	40	45	
Glu Ala Leu Ala Pro Ala Thr Pro Ala Met Pro Arg Ala Pro Arg Cys	50	55	60	
Arg Ala Val Arg Ser Leu Leu Arg Ser His Tyr Arg Glu Val Leu Pro	65	70	75	80
Leu Ala Thr Phe Val Arg Arg Leu Gly Pro Gln Gly Trp Arg Leu Val	85	90	95	
Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala Leu Val Ala Gln Cys Leu	100	105	110	
Val Cys Val Pro Trp Asp Ala Arg Pro Pro Pro Ala Ala Pro Ser Phe	115	120	125	
Arg Gln Val Ser Cys Leu Lys Glu Leu Val Ala Arg Val Leu Gln Arg	130	135	140	
Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe Gly Phe Ala Leu	145	150	155	160
Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe Thr Thr Ser Val	165	170	175	
Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu Arg Gly Ser Gly	180	185	190	
Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp Val Leu Val His	195	200	205	
Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala Pro Ser Cys Ala	210	215	220	

Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly Ala Ala Thr Gln
 225 230 235 240
 Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg Arg Leu Gly Cys
 245 250 255
 Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly Val Pro Leu Gly
 260 265 270
 Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser Ala Ser Arg Ser
 275 280 285
 Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala Pro Glu Pro Glu
 290 295 300
 Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro Gly Arg Thr Arg
 305 310 315 320
 Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro Ala Arg Pro Ala
 325 330 335
 Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly Thr Arg His Ser
 340 345 350
 His Pro Ser Val Gly Arg Gln His His Ala Gly Pro Pro Ser Thr Ser
 355 360 365
 Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu
 370 375 380
 Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro
 385 390 395 400
 Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg
 405 410 415
 Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp Met Pro Gly Thr
 420 425 430
 Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp Gln Met Arg Pro
 435 440 445
 Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys Pro Tyr Gly Val
 450 455 460
 Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val Thr Pro Ala Ala
 465 470 475 480
 Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val Ala Ala Pro Glu
 485 490 495
 Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu Leu Arg Gln His
 500 505 510
 Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg
 515 520 525
 Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn Glu Arg Arg Phe
 530 535 540

Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys His Ala Lys Leu
 545 550 555 560

Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg Asp Cys Ala Trp
 565 570 575

Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala Ala Glu His Arg
 580 585 590

Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp Leu Met Ser Val
 595 600 605

Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr
 610 615 620

Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys
 625 630 635 640

Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg
 645 650 655

Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu Ala Arg Pro Ala
 660 665 670

Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg
 675 680 685

Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg
 690 695 700

Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys Ala Leu Phe Ser
 705 710 715 720

Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser
 725 730 735

Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu
 740 745 750

Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr Phe Val Lys Val
 755 760 765

Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu
 770 775 780

Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg
 785 790 795 800

Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe
 805 810 815

Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln
 820 825 830

Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val
 835 840 845

Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp
 850 855 860

Val Phe Leu Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys
 865 870 875 880
 Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr
 885 890 895
 Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala
 900 905 910
 Gly Ile Arg Arg Asp Gly Leu Leu Arg Leu Val Asp Asp Phe Leu
 915 920 925
 Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu
 930 935 940
 Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr
 945 950 955 960
 Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe
 965 970 975
 Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu
 980 985 990
 Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg
 995 1000 1005
 Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly
 1010 1015 1020
 Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His
 1025 1030 1035 1040
 Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr
 1045 1050 1055
 Asn Ile Tyr Lys Ile Leu Leu Gln Ala Tyr Arg Phe His Ala Cys
 1060 1065 1070
 Val Leu Gln Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe
 1075 1080 1085
 Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu
 1090 1095 1100
 Lys Ala Lys Asn Ala Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly
 1105 1110 1115 1120
 Pro Leu Pro Ser Glu Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu
 1125 1130 1135
 Leu Lys Leu Thr Arg His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser
 1140 1145 1150
 Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr
 1155 1160 1165
 Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe
 1170 1175 1180

Lys Thr Ile Leu Asp
1185

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Xaa Arg Xaa Ile Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Xaa Xaa Xaa Xaa Phe Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Tyr Asp Xaa
1 5 10 15

Xaa

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 92 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

CTGCCCTCAG ACTTCAAGAC CATCCTGGAC TACAAGGACG ACGATGACAA ATGAATTCAAG 60

ATCTGCGGCC GCCACCGCGG TGGAGCTCCA GC 92

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Tyr Xaa Xaa Xaa Xaa Gly Xaa Xaa Gln Gly Xaa Xaa Xaa Ser Xaa Xaa
1 5 10 15
Xaa Xaa Xaa Xaa Xaa Xaa
20

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

Xaa Xaa Xaa Xaa Xaa Xaa Asp Asp Xaa Leu Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

TTYTTYTAYG TNACNGA

17

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

TCNGTNACRT ARAARAA

17

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

MGNNTTYATHC CNAARCC

17

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GCCACCCCCG CGCTGCCTCG AGCTCCCCGC TGC

33

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Pro Gln Asn Pro Lys Thr Pro Lys Pro Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Lys Lys Lys Lys Leu Arg
1 5

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Phe Arg Asn Lys Ile Leu Phe Pro His Lys Trp Arg Trp Ile Leu Ile
1 5 10 15
Trp Met Ile

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Lys Ile Tyr Phe Leu Ile His Ser Thr Ser Ile Ala Ala Leu Val Val
1 5 10 15
Thr Arg Lys Asp Ala Lys His Cys Asn Leu Ala Arg Asn Arg Leu His
20 25 30
Cys Leu Phe Gln Ser Cys Lys Asn Asn
35 40

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Ser Ser Thr Ser Arg Met Gln Ile Phe Ile Thr Ile Leu Ser Cys Glu
1 5 10 15

Asn

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

Lys Ala Glu Ser Lys Glu
1 5

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Lys Leu Lys His Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

Cys Leu Asn Lys Ile Arg
1 5

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Cys Gly Leu Phe Tyr Phe Leu Asp His Phe Leu Arg Ser Ile Met Glu
1 5 10 15
Lys Ile Thr

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Lys Val Asn Ser Leu Asp Tyr Phe Pro Ser Gln Gln Cys Cys Val Tyr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Ile His Met Arg Met Ser Gln Arg Ile Ser Ile His Gln Thr Tyr Gln
1 5 10 15

Arg Gln Thr Arg Tyr Lys Thr Gln Glu Lys Val Cys
20 25

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

Ser Asn Ser Arg Arg Thr Tyr Cys Ile Tyr Tyr Ser Tyr Gly Phe Tyr
1 5 10 15

Tyr Asn Cys Phe Arg Tyr Arg Arg Cys Thr Pro Glu Ser Cys Asp Asn
20 25 30

Cys Lys Ser Cys Leu Gln Leu Lys Glu Ser Gln Phe Cys Lys Phe Cys
35 40 45

Cys Val Cys His Tyr Phe Val Asn
50 55

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 134 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Ser Gln Ile Ser Tyr Leu Asn Leu Met Asp Ser Tyr Arg Asn Lys Pro
1 5 10 15

Asn Lys Pro Cys Lys Phe Asn Gly Ile Tyr Val Lys Ser Phe Gly Thr
20 25 30

Asn Ala His Cys Ile Tyr Ile Gly Phe Leu Lys His Arg Tyr Thr Glu
35 40 45

Cys Phe Arg Asp Cys Phe Ser Leu Gln Gln Ile Thr Cys Phe Asp Tyr
50 55 60

Ser Cys Ser Ser Leu Ile Ser Leu Lys Glu Ala Gly Glu Met Lys Arg
65 70 75 80

Arg Leu Lys Lys Glu Ile Ser Lys Phe Val Asp Ser Ser Val Thr Gly
85 90 95

Ile Asn Asn Lys Asn Ile Ser Asn Glu Lys Glu Glu Glu Leu Ser Gln
100 105 110
Ser Cys Phe Leu Lys Ile Ser Lys Ile Pro Gly Lys Arg Asp Thr Phe
115 120 125
Ile Lys Ile His Ile Leu
130

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

Phe Phe Ile Ser Gln Leu Leu Phe Ser Phe Ile Leu Thr Ile Phe Phe
1 5 10 15

Asp

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Leu Glu Val Lys Ser Ile Lys
1 5

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

Thr Glu Val Thr
1

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Leu Ile His Ile His Arg Ser Thr Phe Ile Tyr Pro Ile Arg Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

Gly Asn Ser Ser His Pro Phe
1 5

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Cys Tyr Glu Asp
1

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Ile	Phe	Arg	Val	Lys	Lys	Trp	Ser	Arg	Asn	Leu	Asn	Gln	Lys	Glu	Leu
1				5					10					15	
Arg	Arg	Tyr	Cys	Lys	Arg	Ile	Glu	Leu							
				20					25						

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Val	Leu	Pro	Ile	Leu	Ile	Asp	Cys	Arg	Asp	Cys	Arg	Gly	Asn	Cys	Thr
1				5					10					15	
Glu	Asp	His													

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

Arg	Asn	Lys	Val	Thr	Phe	Ile	Asn								
1				5											

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Ile	Thr	Asn	Ile	Glu	Ile	Ser	Asp	Leu	Gln	Leu	Thr	Lys			
1				5					10						

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

Thr	Ile	Lys	Asn	Thr	Asn	Leu	Gly	Gln	Asn	Ile	Glu	Glu	Gly	Lys	Glu
1					5				10					15	
Asp	Gln	Leu	Ala	Lys	Glu	Lys	Ile	Arg	Gln						
		20					25								

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Ile	Lys	Cys	Val	Gln	Lys	Cys	Arg	Asn	Lys	Arg	Phe	Ile	Phe	Phe	Asn
1					5				10					15	
Asn	Leu	Leu	Lys	Arg	Gly	Val	Leu	Gly	Phe	Trp	Gly	Phe	Gly		
		20				25							30		

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

Pro	Lys	Thr	Pro	Lys	Pro	Gln	Asn	Pro	Tyr	Lys	Lys	Arg	Lys	Asn	Cys
1					5				10					15	
Gly	Ser	Leu	Glu	Ile	Lys	Tyr	Tyr	Ser	Arg	Thr	Asn	Gly	Asp	Gly	Tyr
		20				25							30		
Cys	Phe	Gly	Cys	Tyr	Arg	Lys	Phe	Thr	Ser						
			35				40								

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Tyr Ile Gln Gln Val
1 5

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

Cys Gln Glu Arg Met Gln Asn Ile Glu Ile Trp Leu Glu Ile Ala Phe
1 5 10 15

Ile Asp Tyr Ser Lys Val Ala Lys Thr Ile Arg Val Leu Leu Leu Gly
20 25 30

Cys Lys Ser Leu
35

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Arg Phe Phe Leu Glu Lys Ile Ser Phe Lys Lys Arg Arg Ala Lys Ser
1 5 10 15

Arg Asn Cys Asn Ile Thr Asn Val
20

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

Ile Lys Ser Gly Asn Glu Asp Tyr Ser Ile Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Gly Ala Leu Trp Arg Lys Leu Leu Asn Thr Lys Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

Thr Val Trp Ile Ile Ser Leu Ala Asn Asn Asp Glu Tyr Ile Lys Phe
1 5 10 15

Ile Cys Glu Cys Val Lys Gly Ser Arg Tyr Ile Arg Leu Thr Lys Asp
20 25 30

Lys Leu Ala Ile Lys Arg Lys Lys Phe Asp Asn Arg Thr Ala Glu
35 40 45

Glu Leu Ile Ala Phe Thr Ile Arg Met Gly Phe Ile Thr Ile Val Leu
50 55 60

Gly Ile Asp Gly Glu Leu Pro Ser Leu Glu Thr Ile Glu Lys Ala Val
65 70 75 80

Tyr Asn Cys Arg Asn Arg Ser Ser Glu Ser Ser Asp Val Tyr Ala Ile
85 90 95
Ile Leu Cys Ile Asn Leu Lys Tyr Leu Ile Ser Ile
100 105

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Trp Ile Ala Ile Glu Thr Asn Gln Ile Asn His Ala Ser Leu Met Glu
1 5 10 15
Tyr Thr Leu Asn Pro Leu Gly Gln Met His Thr Glu Phe Ile Leu Asp
20 25 30
Ser

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Ser Ile Asp Thr Gln Asn Ala Leu Glu Thr Asp Leu Ala Tyr Asn Arg
1 5 10 15
Leu Pro Val Leu Ile Thr Leu Ala His Leu Leu Tyr Leu
20 25

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Lys Lys Gln Ala Lys Cys Lys Glu Asp
1 5

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Arg Lys Arg Phe Gln Asn Leu Leu Ile Leu Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Pro Glu Leu Thr Thr Arg Ile Leu Ala Thr Lys Lys Lys Lys Ser Tyr
1 5 10 15
His Asn Pro Asp Ser
20

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

Arg Phe Gln Lys Phe Gln Val Arg Glu Ile His Ser Leu Lys Phe Ile
1 5 10 15
Tyr Tyr Ser Phe Ser Phe His Ser Cys Tyr Phe Leu Leu Ser
20 25 30

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Gln Tyr Phe Leu Ile Ser Trp Lys
1 5

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

Lys Val Ser Asn Lys Arg Ser Ala Arg Leu Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Leu Ser Leu Phe Thr Phe Ile Asp Arg Pro Ser Tyr Ile Gln Tyr Asp
1 5 10 15

Asp Lys Glu Thr Ala Val Ile Arg Phe Lys Asn Ser Ala Met Arg Thr
20 25 30

Lys Phe Leu Glu Ser Arg Asn Gly Ala Glu Ile Leu Ile Lys Lys Asn
35 40 45

Cys Val Asp Ile Ala Lys Glu Ser Asn Ser Lys Ser Phe Val Asn Lys
50 55 60

Tyr Tyr Gln Ser Cys Leu Ile Glu Glu Ile Asp Glu Ala Thr Ala Gln
65 70 75 80

Lys Ile Ile Lys Glu Ile Lys
85

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

Leu Leu Leu Ile Arg Glu
1 5

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Thr Lys Leu Leu Ile
1 5

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

Arg Ser Ala Ile Phe Asn Cys Arg Asn Lys Ser Cys Thr Lys Val Arg
1 5 10 15

Gln

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Lys Ile Gln Thr Leu Val Lys Ile Leu Arg Lys Glu Lys Lys Thr Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

Gln Lys Lys Lys
1

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Asn Glu Tyr Arg Ser Glu Glu Ile Lys Asp Leu Phe Phe Ser Ile Ile
1 5 10 15

Tyr Cys Lys Glu Gly Phe Trp Gly Phe Gly Val Leu Gly
20 25

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

Pro	Lys	Pro	Gln	Asn	Pro	Lys	Thr	Pro	Ile	Lys	Lys	Glu	Lys	Ile	Glu
1					5					10					15
Val	Val														

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

Asn	Ile	Ile	Pro	Ala	Gln	Met	Glu	Met	Asp	Ile	Asp	Leu	Asp	Asp	Ile
1						5				10					15
Glu	Asn	Leu	Leu	Pro	Asn	Thr	Phe	Asn	Lys	Tyr	Ser	Ser	Ser	Cys	Ser
	20							25						30	
Asp	Lys	Lys	Gly	Cys	Lys	Thr	Leu	Lys	Ser	Gly	Ser	Lys	Ser	Pro	Ser
	35						40					45			
Leu	Thr	Ile	Pro	Lys	Leu	Gln	Lys	Gln	Leu	Glu	Phe	Tyr	Phe	Ser	Asp
	50				55					60					
Ala	Asn	Leu	Tyr	Asn	Asp	Ser	Phe	Leu	Arg	Lys	Leu	Val	Leu	Lys	Ser
	65					70			75					80	
Gly	Glu	Gln	Arg	Val	Glu	Ile	Glu	Thr	Leu	Leu	Met	Phe	Lys		
				85					90						

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

Asn	Gln	Val	Met	Arg	Ile	Ile	Leu	Phe	Phe	Arg	Ser	Leu	Leu	Lys	Glu
1					5					10					15

His Tyr Gly Glu Asn Tyr Leu Ile Leu Lys Gly Lys Gln Phe Gly Leu
20 25 30
Phe Pro

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Pro Thr Met Met Ser Ile Leu Asn Ser Tyr Glu Asn Glu Ser Lys Asp
1 5 10 15
Leu Asp Thr Ser Asp Leu Pro Lys Thr Asn Ser Leu
20 25

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

Asn Ala Arg Lys Ser Leu Ile Ile Glu Gln Gln Lys Asn Leu Leu His
1 5 10 15
Leu Leu Phe Val Trp Val Leu Leu Gln Leu Phe
20 25

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Val Ser Thr Val Asn Ser Arg Val Leu Arg Gln Leu Lys Lys Leu Phe
1 5 10 15

Thr Thr Glu Gly Ile Ala Val Leu Lys Val Leu Met Cys Met Pro Leu
20 25 30

Phe Cys Glu Leu Ile Ser Asn Ile Leu Ser Gln Phe Asn Gly
35 40 45

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

Lys Gln Thr Lys
1

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Thr Met Gln Val
1

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

Trp Asn Ile Arg
1

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Ile Leu Trp Asp Lys Cys Thr Leu Asn Leu Tyr Trp Ile Leu Lys Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

Ile His Arg Met Leu
1 5

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Leu Thr Thr Asp Tyr Leu Phe Cys Leu Leu Leu Leu Ile Ser Tyr Ile
1 5 10 15

Phe Lys Arg Ser Arg Arg Asn Glu Lys Lys Thr Lys Glu Arg Asp Phe
20 25 30

Lys Ile Cys Cys Phe Phe Cys Asn Arg Asn
35 40

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

Gln Gln Glu Tyr
1

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Gln Arg Lys Arg Arg Arg Ala Ile Thr Ile Leu Ile Leu Lys Asp Phe
1 5 10 15
Lys Asn Ser Arg
20

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

Glu Arg Tyr Ile His
1 5

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Asn	Ser	Tyr	Ile	Ile	Val	Phe	His	Phe	Thr	Ala	Val	Ile	Phe	Phe	Tyr
1				5					10					15	
Leu	Asn	Asn	Ile	Phe	Cys	Leu	Ala	Gly	Ser	Lys	Lys	Tyr	Gln	Ile	Arg
			20					25					30		
Glu	Ala	Leu	Asp	Cys	Gly	Asn	Leu	Ala	Tyr	Ser	His	Ser			
			35				40				45				

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

Ile	Asp	Leu	His	Ile	Ser	Asn	Thr	Met	Ile	Arg	Lys	Gln	Gln	Ser	Ser
1				5					10					15	
Val	Leu	Lys	Ile	Val	Leu	Cys	Gly	Leu	Asn	Phe					
			20				25								

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

Ser	Gln	Glu	Met	Glu	Pro	Lys	Ser
1			5				

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

Ser Lys Arg Ile Ala Ser Ile Leu Gln Lys Asn Arg Thr Leu Asn Leu
1 5 10 15
Ser Leu Ile Ser Ile Thr Asn Leu Asp Cys Leu Lys Arg Leu Thr Arg
20 25 30
Gln Leu His Arg Arg Ser Leu Lys Lys
35 40

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Ser Asn Phe Tyr
1

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

Leu Glu Asn Lys Leu Asn Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Tyr Arg Asp Gln Arg Ser Ser Ile Asp Glu Ile Lys Ala Glu Leu Lys
1 5 10 15

Leu Asp Asn Lys Lys Tyr Lys Pro Trp Ser Lys Tyr Cys Gly Arg Lys
20 25 30

Arg Arg Pro Val Ser Lys Arg Lys Asn Ala Ile Asn Lys Met Ser
35 40 45

Thr Glu Val Lys Lys
50

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

Lys Ile Tyr Phe Phe Gln
1 5

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Phe Ile Glu Lys Arg Gly Phe Gly Val Leu Gly Phe Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1007 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

Glu Val Asp Val Asp Asn Gln Ala Asp Asn His Gly Ile His Ser Ala
1 5 10 15

Leu Lys Thr Cys Glu Glu Ile Lys Glu Ala Lys Thr Leu Tyr Ser Trp
 20 25 30

Ile Gln Lys Val Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr Lys
 35 40 45

Asp Leu Glu Asp Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala Thr
 50 55 60

Pro Arg Asp Tyr Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys Glu
 65 70 75 80

Val Phe Ser Thr Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu Val
 85 90 95

Glu Leu Leu Ser Ser Ser Asp Val Ser Asp Arg Gln Lys Leu Gln Cys
 100 105 110

Phe Gly Phe Gln Leu Lys Gly Asn Gln Leu Ala Lys Thr His Leu Leu
 115 120 125

Thr Ala Leu Ser Thr Gln Lys Gln Tyr Phe Phe Gln Asp Glu Trp Asn
 130 135 140

Gln Val Arg Ala Met Ile Gly Asn Glu Leu Phe Arg His Leu Tyr Thr
 145 150 155 160

Lys Tyr Leu Ile Phe Gln Arg Thr Ser Glu Gly Thr Leu Val Gln Phe
 165 170 175

Cys Gly Asn Asn Val Phe Asp His Leu Lys Val Asn Asp Lys Phe Asp
 180 185 190

Lys Lys Gln Lys Gly Gly Ala Ala Asp Met Asn Glu Pro Arg Cys Cys
 195 200 205

Ser Thr Cys Lys Tyr Asn Val Lys Asn Glu Lys Asp His Phe Leu Asn
 210 215 220

Asn Ile Asn Val Pro Asn Trp Asn Asn Met Lys Ser Arg Thr Arg Ile
 225 230 235 240

Phe Tyr Cys Thr His Phe Asn Arg Asn Asn Gln Phe Phe Lys Lys His
 245 250 255

Glu Phe Val Ser Asn Lys Asn Asn Ile Ser Ala Met Asp Arg Ala Gln
 260 265 270

Thr Ile Phe Thr Asn Ile Phe Arg Phe Asn Arg Ile Arg Lys Lys Leu
 275 280 285

Lys Asp Lys Val Ile Glu Lys Ile Ala Tyr Met Leu Glu Lys Val Lys
 290 295 300

Asp Phe Asn Phe Asn Tyr Tyr Leu Thr Lys Ser Cys Pro Leu Pro Glu
 305 310 315 320

Asn Trp Arg Glu Arg Lys Gln Lys Ile Glu Asn Leu Ile Asn Lys Thr
 325 330 335

Arg Glu Glu Lys Ser Lys Tyr Tyr Glu Glu Leu Phe Ser Tyr Thr Thr
 340 345 350

Asp Asn Lys Cys Val Thr Gln Phe Ile Asn Glu Phe Phe Tyr Asn Ile
 355 360 365

Leu Pro Lys Asp Phe Leu Thr Gly Arg Asn Arg Lys Asn Phe Gln Lys
 370 375 380

Lys Val Lys Lys Tyr Val Glu Leu Asn Lys His Glu Leu Ile His Lys
 385 390 395 400

Asn Leu Leu Leu Glu Lys Ile Asn Thr Arg Glu Ile Ser Trp Met Gln
 405 410 415

Val Glu Thr Ser Ala Lys His Phe Tyr Tyr Phe Asp His Glu Asn Ile
 420 425 430

Tyr Val Leu Trp Lys Leu Leu Arg Trp Ile Phe Glu Asp Leu Val Val
 435 440 445

Ser Leu Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser Tyr
 450 455 460

Ser Lys Thr Tyr Tyr Arg Lys Asn Ile Trp Asp Val Ile Met Lys
 465 470 475 480

Met Ser Ile Ala Asp Leu Lys Lys Glu Thr Leu Ala Glu Val Gln Glu
 485 490 495

Lys Glu Val Glu Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly Lys
 500 505 510

Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr Phe
 515 520 525

Asn Lys Lys Ile Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr Thr
 530 535 540

Asn Thr Lys Leu Leu Asn Ser His Leu Met Leu Lys Thr Leu Lys Asn
 545 550 555 560

Arg Met Phe Lys Asp Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp Asp
 565 570 575

Val Met Lys Lys Tyr Glu Glu Phe Val Cys Lys Trp Lys Gln Val Gly
 580 585 590

Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp
 595 600 605

Ser Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys Leu
 610 615 620

Leu Ser Ser Asp Phe Trp Ile Met Thr Ala Gln Ile Leu Lys Arg Lys
 625 630 635 640

Asn Asn Ile Val Ile Asp Ser Lys Asn Phe Arg Lys Lys Glu Met Lys
 645 650 655

Asp Tyr Phe Arg Gln Lys Phe Gln Lys Ile Ala Leu Glu Gly Gly Gln
 660 665 670
 Tyr Pro Thr Leu Phe Ser Val Leu Glu Asn Glu Gln Asn Asp Leu Asn
 675 680 685
 Ala Lys Lys Thr Leu Ile Val Glu Ala Lys Gln Arg Asn Tyr Phe Lys
 690 695 700
 Lys Asp Asn Leu Leu Gln Pro Val Ile Asn Ile Cys Gln Tyr Asn Tyr
 705 710 715 720
 Ile Asn Phe Asn Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln
 725 730 735
 Gly Leu Cys Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu
 740 745 750
 Glu Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro Glu
 755 760 765
 Asn Pro Asn Val Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu
 770 775 780
 Ile Thr Thr Gln Glu Asn Asn Ala Val Leu Phe Ile Glu Lys Leu Ile
 785 790 795 800
 Asn Val Ser Arg Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu Gln
 805 810 815
 Thr Ser Phe Pro Leu Ser Pro Ser Lys Phe Ala Lys Tyr Gly Met Asp
 820 825 830
 Ser Val Glu Glu Gln Asn Ile Val Gln Asp Tyr Cys Asp Trp Ile Gly
 835 840 845
 Ile Ser Ile Asp Met Lys Thr Leu Ala Leu Met Pro Asn Ile Asn Leu
 850 855 860
 Arg Ile Glu Gly Ile Leu Cys Thr Leu Asn Leu Asn Met Gln Thr Lys
 865 870 875 880
 Lys Ala Ser Met Trp Leu Lys Lys Lys Leu Lys Ser Phe Leu Met Asn
 885 890 895
 Asn Ile Thr His Tyr Phe Arg Lys Thr Ile Thr Thr Glu Asp Phe Ala
 900 905 910
 Asn Lys Thr Leu Asn Lys Leu Phe Ile Ser Gly Gly Tyr Lys Tyr Met
 915 920 925
 Gln Cys Ala Lys Glu Tyr Lys Asp His Phe Lys Lys Asn Leu Ala Met
 930 935 940
 Ser Ser Met Ile Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val Thr
 945 950 955 960
 Arg Ala Phe Phe Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile Phe
 965 970 975

Gly	Glu	Glu	His	Tyr	Pro	Asp	Phe	Phe	Leu	Ser	Thr	Leu	Lys	His	Phe
980													990		
Ile	Glu	Ile	Phe	Ser	Thr	Lys	Lys	Tyr	Ile	Phe	Asn	Arg	Val	Cys	
995													1005		

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Glu	Leu	Glu	Leu	Glu	Met	Gln	Glu	Asn	Gln	Asn	Asp	Ile	Gln	Val	Arg
1					5				10				15		
Val	Lys	Ile	Asp	Asp	Pro	Lys	Gln	Tyr	Leu	Val	Asn	Val	Thr	Ala	Ala
					20				25				30		
Cys	Leu	Leu	Gln	Glu	Gly	Ser	Tyr	Tyr	Gln	Asp	Lys	Asp	Glu	Arg	Arg
					35				40				45		
Tyr	Ile	Ile	Thr	Lys	Ala	Leu	Leu	Glu	Val	Ala	Glu	Ser	Asp	Pro	Glu
					50				55				60		
Phe	Ile	Cys	Gln	Leu	Ala	Val	Tyr	Ile	Arg	Asn	Glu	Leu	Tyr	Ile	Arg
					65				70				75		80
Thr	Thr	Thr	Asn	Tyr	Ile	Val	Ala	Phe	Cys	Val	Val	His	Lys	Asn	Thr
					85				90				95		
Gln	Pro	Phe	Ile	Glu	Lys	Tyr	Phe	Asn	Lys	Ala	Val	Leu	Leu	Pro	Asn
					100				105				110		
Asp	Leu	Leu	Glu	Val	Cys	Glu	Phe	Ala	Gln	Val	Leu	Tyr	Ile	Phe	Asp
					115				120				125		
Ala	Thr	Glu	Phe	Lys	Asn	Leu	Tyr	Leu	Asp	Arg	Ile	Leu	Ser	Gln	Asp
					130				135				140		
Ile	Arg	Lys	Glu	Leu	Thr	Phe	Arg	Lys	Cys	Leu	Gln	Arg	Cys	Val	Arg
					145				150				155		160
Ser	Lys	Phe	Ser	Glu	Phe	Asn	Glu	Tyr	Gln	Leu	Gly	Lys	Tyr	Cys	Thr
					165				170				175		
Glu	Ser	Gln	Arg	Lys	Lys	Thr	Met	Phe	Arg	Tyr	Leu	Ser	Val	Thr	Asn
					180				185				190		
Lys	Gln	Lys	Trp	Asp	Gln	Thr	Lys	Lys	Lys	Arg	Lys	Glu	Asn	Leu	Leu
					195				200				205		
Thr	Lys	Leu	Gln	Ala	Ile	Lys	Glu	Ser	Glu	Asp	Lys	Ser	Lys	Arg	Glu
					210				215				220		

Thr Gly Asp Ile Met Asn Val Glu Asp Ala Ile Lys Ala Leu Lys Pro
 225 230 235 240
 Ala Val Met Lys Lys Ile Ala Lys Arg Gln Asn Ala Met Lys Lys His
 245 250 255
 Met Lys Ala Pro Lys Ile Pro Asn Ser Thr Leu Glu Ser Lys Tyr Leu
 260 265 270
 Thr Phe Lys Asp Leu Ile Lys Phe Cys His Ile Ser Glu Pro Lys Glu
 275 280 285
 Arg Val Tyr Lys Ile Leu Gly Lys Lys Tyr Pro Lys Thr Glu Glu Glu
 290 295 300
 Tyr Lys Ala Ala Phe Gly Asp Ser Ala Ser Ala Pro Phe Asn Pro Glu
 305 310 315 320
 Leu Ala Gly Lys Arg Met Lys Ile Glu Ile Ser Lys Thr Trp Glu Asn
 325 330 335
 Glu Leu Ser Ala Lys Gly Asn Thr Ala Glu Val Trp Asp Asn Leu Ile
 340 345 350
 Ser Ser Asn Gln Leu Pro Tyr Met Ala Met Leu Arg Asn Leu Ser Asn
 355 360 365
 Ile Leu Lys Ala Gly Val Ser Asp Thr Thr His Ser Ile Val Ile Asn
 370 375 380
 Lys Ile Cys Glu Pro Lys Ala Val Glu Asn Ser Lys Met Phe Pro Leu
 385 390 395 400
 Gln Phe Phe Ser Ala Ile Glu Ala Val Asn Glu Ala Val Thr Lys Gly
 405 410 415
 Phe Lys Ala Lys Lys Arg Glu Asn Met Asn Leu Lys Gly Gln Ile Glu
 420 425 430
 Ala Val Lys Glu Val Val Glu Lys Thr Asp Glu Glu Lys Lys Asp Met
 435 440 445
 Glu Leu Glu Gln Thr Glu Glu Gly Glu Phe Val Lys Val Asn Glu Gly
 450 455 460
 Ile Gly Lys Gln Tyr Ile Asn Ser Ile Glu Leu Ala Ile Lys Ile Ala
 465 470 475 480
 Val Asn Lys Asn Leu Asp Glu Ile Lys Gly His Thr Ala Ile Phe Ser
 485 490 495
 Asp Val Ser Gly Ser Met Ser Thr Ser Met Ser Gly Gly Ala Lys Lys
 500 505 510
 Tyr Gly Ser Val Arg Thr Cys Leu Glu Cys Ala Leu Val Leu Gly Leu
 515 520 525
 Met Val Lys Gln Arg Cys Glu Lys Ser Ser Phe Tyr Ile Phe Ser Ser
 530 535 540

Pro	Ser	Ser	Gln	Cys	Asn	Lys	Cys	Tyr	Leu	Glu	Val	Asp	Leu	Pro	Gly
545										555					560
Asp	Glu	Leu	Arg	Pro	Ser	Met	Gln	Lys	Leu	Leu	Gln	Glu	Lys	Gly	Lys
									565	570					575
Leu	Gly	Gly	Gly	Thr	Asp	Phe	Pro	Tyr	Glu	Cys	Ile	Asp	Glu	Trp	Thr
									580	585					590
Lys	Asn	Lys	Thr	His	Val	Asp	Asn	Ile	Val	Ile	Leu	Ser	Asp	Met	Met
									595	600					605
Ile	Ala	Glu	Gly	Tyr	Ser	Asp	Ile	Asn	Val	Arg	Gly	Ser	Ser	Ile	Val
									610	615					620
Asn	Ser	Ile	Lys	Lys	Tyr	Lys	Asp	Glu	Val	Asn	Pro	Asn	Ile	Lys	Ile
									625	630					640
Phe	Ala	Val	Asp	Leu	Glu	Gly	Tyr	Gly	Lys	Cys	Leu	Asn	Leu	Gly	Asp
									645	650					655
Glu	Phe	Asn	Glu	Asn	Asn	Tyr	Ile	Lys	Ile	Phe	Gly	Met	Ser	Asp	Ser
									660	665					670
Ile	Leu	Lys	Phe	Ile	Ser	Ala	Lys	Gln	Gly	Gly	Ala	Asn	Met	Val	Glu
									675	680					685
Val	Ile	Lys	Asn	Phe	Ala	Leu	Gln	Lys	Ile	Gly					
									690	695					

(2) INFORMATION FOR SEQ ID NO:225:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 897 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

Leu	Ser	Thr	Gln	Lys	Gln	Tyr	Phe	Phe	Gln	Asp	Glu	Trp	Asn	Gln	Val
1															15
Arg	Ala	Met	Ile	Gly	Asn	Glu	Leu	Phe	Arg	His	Leu	Tyr	Thr	Lys	Tyr
			20						25					30	
Leu	Ile	Phe	Gln	Arg	Thr	Ser	Glu	Gly	Thr	Leu	Val	Gln	Phe	Cys	Gly
			35						40					45	
Asn	Asn	Val	Phe	Asp	His	Leu	Lys	Val	Asn	Asp	Lys	Phe	Asp	Lys	Lys
			50						55					60	
Gln	Lys	Gly	Gly	Ala	Ala	Asp	Met	Asn	Glu	Pro	Arg	Cys	Cys	Ser	Thr
									65						80
Cys	Lys	Tyr	Asn	Val	Lys	Asn	Glu	Lys	Asp	His	Phe	Leu	Asn	Asn	Ile
									85						95
									90						

Asn	Val	Pro	Asn	Trp	Asn	Asn	Met	Lys	Ser	Arg	Thr	Arg	Ile	Phe	Tyr
							100		105				110		
Cys	Thr	His	Phe	Asn	Arg	Asn	Asn	Gln	Phe	Phe	Lys	Lys	His	Glu	Phe
							115		120				125		
Val	Ser	Asn	Lys	Asn	Asn	Ile	Ser	Ala	Met	Asp	Arg	Ala	Gln	Thr	Ile
						130		135				140			
Phe	Thr	Asn	Ile	Phe	Arg	Phe	Asn	Arg	Ile	Arg	Lys	Lys	Leu	Lys	Asp
						145		150			155		160		
Lys	Val	Ile	Glu	Lys	Ile	Ala	Tyr	Met	Leu	Glu	Lys	Val	Lys	Asp	Phe
						165			170			175			
Asn	Phe	Asn	Tyr	Tyr	Leu	Thr	Lys	Ser	Cys	Pro	Leu	Pro	Glu	Asn	Trp
						180			185			190			
Arg	Glu	Arg	Lys	Gln	Lys	Ile	Glu	Asn	Leu	Ile	Asn	Lys	Thr	Arg	Glu
						195			200			205			
Glu	Lys	Ser	Lys	Tyr	Tyr	Glu	Glu	Leu	Phe	Ser	Tyr	Thr	Thr	Asp	Asn
						210			215			220			
Lys	Cys	Val	Thr	Gln	Phe	Ile	Asn	Glu	Phe	Phe	Tyr	Asn	Ile	Leu	Pro
						225			230			235			240
Lys	Asp	Phe	Leu	Thr	Gly	Arg	Asn	Arg	Lys	Asn	Phe	Gln	Lys	Lys	Val
						245			250			255			
Lys	Lys	Tyr	Val	Glu	Leu	Asn	Lys	His	Glu	Leu	Ile	His	Lys	Asn	Leu
						260			265			270			
Leu	Leu	Glu	Lys	Ile	Asn	Thr	Arg	Glu	Ile	Ser	Trp	Met	Gln	Val	Glu
						275			280			285			
Thr	Ser	Ala	Lys	His	Phe	Tyr	Tyr	Phe	Asp	His	Glu	Asn	Ile	Tyr	Val
						290			295			300			
Leu	Trp	Lys	Leu	Leu	Arg	Trp	Ile	Phe	Glu	Asp	Leu	Val	Val	Ser	Leu
						305			310			315			320
Ile	Arg	Cys	Phe	Phe	Tyr	Val	Thr	Glu	Gln	Gln	Lys	Ser	Tyr	Ser	Lys
						325			330			335			
Thr	Tyr	Tyr	Tyr	Arg	Lys	Asn	Ile	Trp	Asp	Val	Ile	Met	Lys	Met	Ser
						340			345			350			
Ile	Ala	Asp	Leu	Lys	Lys	Glu	Thr	Leu	Ala	Glu	Val	Gln	Glu	Lys	Glu
						355			360			365			
Val	Glu	Glu	Trp	Lys	Lys	Ser	Leu	Gly	Phe	Ala	Pro	Gly	Lys	Leu	Arg
						370			375			380			
Leu	Ile	Pro	Lys	Lys	Thr	Thr	Phe	Arg	Pro	Ile	Met	Thr	Phe	Asn	Lys
						385			390			395			400
Lys	Ile	Val	Asn	Ser	Asp	Arg	Lys	Thr	Thr	Lys	Leu	Thr	Thr	Asn	Thr
						405			410			415			

Lys Leu Leu Asn Ser His Leu Met Leu Lys Thr Leu Lys Asn Arg Met
 420 425 430
 Phe Lys Asp Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp Asp Val Met
 435 440 445
 Lys Lys Tyr Glu Glu Phe Val Cys Lys Trp Lys Gln Val Gly Gln Pro
 450 455 460
 Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp Ser Val
 465 470 475 480
 Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys Leu Leu Ser
 485 490 495
 Ser Asp Phe Trp Ile Met Thr Ala Gln Ile Leu Lys Arg Lys Asn Asn
 500 505 510
 Ile Val Ile Asp Ser Lys Asn Phe Arg Lys Lys Glu Met Lys Asp Tyr
 515 520 525
 Phe Arg Gln Lys Phe Gln Lys Ile Ala Leu Glu Gly Gly Gln Tyr Pro
 530 535 540
 Thr Leu Phe Ser Val Leu Glu Asn Glu Gln Asn Asp Leu Asn Ala Lys
 545 550 555 560
 Lys Thr Leu Ile Val Glu Ala Lys Gln Arg Asn Tyr Phe Lys Lys Asp
 565 570 575
 Asn Leu Leu Gln Pro Val Ile Asn Ile Cys Gln Tyr Asn Tyr Ile Asn
 580 585 590
 Phe Asn Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu
 595 600 605
 Cys Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu Glu
 610 615 620
 Ser Ser Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro Glu Asn Pro
 625 630 635 640
 Asn Val Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile Thr
 645 650 655
 Thr Gln Glu Asn Asn Ala Val Leu Phe Ile Glu Lys Leu Ile Asn Val
 660 665 670
 Ser Arg Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu Gln Thr Ser
 675 680 685
 Phe Pro Leu Ser Pro Ser Lys Phe Ala Lys Tyr Gly Met Asp Ser Val
 690 695 700
 Glu Glu Gln Asn Ile Val Gln Asp Tyr Cys Asp Trp Ile Gly Ile Ser
 705 710 715 720
 Ile Asp Met Lys Thr Leu Ala Leu Met Pro Asn Ile Asn Leu Arg Ile
 725 730 735

Glu Gly Ile Leu Cys Thr Leu Asn Leu Asn Met Gln Thr Lys Lys Ala
 740 745 750
 Ser Met Trp Leu Lys Lys Lys Leu Lys Ser Phe Leu Met Asn Asn Ile
 755 760 765
 Thr His Tyr Phe Arg Lys Thr Ile Thr Thr Glu Asp Phe Ala Asn Lys
 770 775 780
 Thr Leu Asn Lys Leu Phe Ile Ser Gly Gly Tyr Lys Tyr Met Gln Cys
 785 790 795 800
 Ala Lys Glu Tyr Lys Asp His Phe Lys Lys Asn Leu Ala Met Ser Ser
 805 810 815
 Met Ile Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val Thr Arg Ala
 820 825 830
 Phe Phe Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile Phe Gly Glu
 835 840 845
 Glu His Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His Phe Ile Glu
 850 855 860
 Ile Phe Ser Thr Lys Lys Tyr Ile Phe Asn Arg Val Cys Met Ile Leu
 865 870 875 880
 Lys Ala Lys Glu Ala Lys Leu Lys Ser Asp Gln Cys Gln Ser Leu Ile
 885 890 895
 Gln

(2) INFORMATION FOR SEQ ID NO:226:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 840 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

Met Ser Arg Arg Asn Gln Lys Lys Pro Gln Ala Pro Ile Gly Asn Glu
 1 5 10 15
 Thr Asn Leu Asp Phe Val Leu Gln Asn Leu Glu Val Tyr Lys Ser Gln
 20 25 30
 Ile Glu His Tyr Lys Thr Gln Gln Gln Ile Lys Glu Glu Asp Leu
 35 40 45
 Lys Leu Leu Lys Phe Lys Asn Gln Asp Gln Asp Gly Asn Ser Gly Asn
 50 55 60
 Asp Asp Asp Asp Glu Glu Asn Asn Ser Asn Lys Gln Gln Glu Leu Leu
 65 70 75 80

Arg	Arg	Val	Asn	Gln	Ile	Lys	Gln	Gln	Val	Gln	Leu	Ile	Lys	Lys	Val
					85					90				95	
Gly	Ser	Lys	Val	Glu	Lys	Asp	Leu	Asn	Leu	Asn	Glu	Asp	Glu	Asn	Lys
					100				105				110		
Lys	Asn	Gly	Leu	Ser	Glu	Gln	Gln	Val	Lys	Glu	Glu	Gln	Leu	Arg	Thr
					115			120				125			
Ile	Thr	Glu	Glu	Gln	Val	Lys	Tyr	Gln	Asn	Leu	Val	Phe	Asn	Met	Asp
					130		135				140				
Tyr	Gln	Leu	Asp	Leu	Asn	Glu	Ser	Gly	Gly	His	Arg	Arg	His	Arg	Arg
					145		150			155			160		
Glu	Thr	Asp	Tyr	Asp	Thr	Glu	Lys	Trp	Phe	Glu	Ile	Ser	His	Asp	Gln
					165			170			175				
Lys	Asn	Tyr	Val	Ser	Ile	Tyr	Ala	Asn	Gln	Lys	Thr	Ser	Tyr	Cys	Trp
					180			185				190			
Trp	Leu	Lys	Asp	Tyr	Phe	Asn	Lys	Asn	Asn	Tyr	Asp	His	Leu	Asn	Val
					195		200				205				
Ser	Ile	Asn	Arg	Leu	Glu	Thr	Glu	Ala	Glu	Phe	Tyr	Ala	Phe	Asp	Asp
					210		215			220					
Phe	Ser	Gln	Thr	Ile	Lys	Leu	Thr	Asn	Asn	Ser	Tyr	Gln	Thr	Val	Asn
					225		230			235			240		
Ile	Asp	Val	Asn	Phe	Asp	Asn	Asn	Leu	Cys	Ile	Leu	Ala	Leu	Leu	Arg
					245			250			255				
Phe	Leu	Leu	Ser	Leu	Glu	Arg	Phe	Asn	Ile	Leu	Asn	Ile	Arg	Ser	Ser
					260			265			270				
Tyr	Thr	Arg	Asn	Gln	Tyr	Asn	Phe	Glu	Lys	Ile	Gly	Glu	Leu	Leu	Glu
					275		280			285					
Thr	Ile	Phe	Ala	Val	Val	Phe	Ser	His	Arg	His	Leu	Gln	Gly	Ile	His
					290		295			300					
Leu	Gln	Val	Pro	Cys	Glu	Ala	Phe	Gln	Tyr	Leu	Val	Asn	Ser	Ser	Ser
					305		310			315			320		
Gln	Ile	Ser	Val	Lys	Asp	Ser	Gln	Leu	Gln	Val	Tyr	Ser	Phe	Ser	Thr
					325			330			335				
Asp	Leu	Lys	Leu	Val	Asp	Thr	Asn	Lys	Val	Gln	Asp	Tyr	Phe	Lys	Phe
					340			345			350				
Leu	Gln	Glu	Phe	Pro	Arg	Leu	Thr	His	Val	Ser	Gln	Gln	Ala	Ile	Pro
					355			360			365				
Val	Ser	Ala	Thr	Asn	Ala	Val	Glu	Asn	Leu	Asn	Val	Leu	Leu	Lys	Lys
					370			375			380				
Val	Lys	His	Ala	Asn	Leu	Asn	Leu	Val	Ser	Ile	Pro	Thr	Gln	Phe	Asn
					385			390			395			400	

Phe Asp Phe Tyr Phe Val Asn Leu Gln His Leu Lys Leu Glu Phe Gly
 405 410 415
 Leu Glu Pro Asn Ile Leu Thr Lys Gln Lys Leu Glu Asn Leu Leu Leu
 420 425 430
 Ser Ile Lys Gln Ser Lys Asn Leu Lys Phe Leu Arg Leu Asn Phe Tyr
 435 440 445
 Thr Tyr Val Ala Gln Glu Thr Ser Arg Lys Gln Ile Leu Lys Gln Ala
 450 455 460
 Thr Thr Ile Lys Asn Leu Lys Asn Asn Lys Asn Gln Glu Glu Thr Pro
 465 470 475 480
 Glu Thr Lys Asp Glu Thr Pro Ser Glu Ser Thr Ser Gly Met Lys Phe
 485 490 495
 Phe Asp His Leu Ser Glu Leu Thr Glu Leu Glu Asp Phe Ser Val Asn
 500 505 510
 Leu Gln Ala Thr Gln Glu Ile Tyr Asp Ser Leu His Lys Leu Leu Ile
 515 520 525
 Arg Ser Thr Asn Leu Lys Phe Lys Leu Ser Tyr Lys Tyr Glu Met
 530 535 540
 Glu Lys Ser Lys Met Asp Thr Phe Ile Asp Leu Lys Asn Ile Tyr Glu
 545 550 555 560
 Thr Leu Asn Asn Leu Lys Arg Cys Ser Val Asn Ile Ser Asn Pro His
 565 570 575
 Gly Asn Ile Ser Tyr Glu Leu Thr Asn Lys Asp Ser Thr Phe Tyr Lys
 580 585 590
 Phe Lys Leu Thr Leu Asn Gln Glu Leu Gln His Ala Lys Tyr Thr Phe
 595 600 605
 Lys Gln Asn Glu Phe Gln Phe Asn Asn Val Lys Ser Ala Lys Ile Glu
 610 615 620
 Ser Ser Ser Leu Glu Ser Leu Glu Asp Ile Asp Ser Leu Cys Lys Ser
 625 630 635 640
 Ile Ala Ser Cys Lys Asn Leu Gln Asn Val Asn Ile Ile Ala Ser Leu
 645 650 655
 Leu Tyr Pro Asn Asn Ile Gln Lys Asn Pro Phe Asn Lys Pro Asn Leu
 660 665 670
 Leu Phe Phe Lys Gln Phe Glu Gln Leu Lys Asn Leu Glu Asn Val Ser
 675 680 685
 Ile Asn Cys Ile Leu Asp Gln His Ile Leu Asn Ser Ile Ser Glu Phe
 690 695 700
 Leu Glu Lys Asn Lys Lys Ile Lys Ala Phe Ile Leu Lys Arg Tyr Tyr
 705 710 715 720

Leu Leu Gln Tyr Tyr Leu Asp Tyr Thr Lys Leu Phe Lys Thr Leu Gln
 725 730 735
 Gln Leu Pro Glu Leu Asn Gln Val Tyr Ile Asn Gln Gln Leu Glu Glu
 740 745 750
 Leu Thr Val Ser Glu Val His Lys Gln Val Trp Glu Asn His Lys Gln
 755 760 765
 Lys Ala Phe Tyr Glu Pro Leu Cys Glu Phe Ile Lys Glu Ser Ser Gln
 770 775 780
 Thr Leu Gln Leu Ile Asp Phe Asp Gln Asn Thr Val Ser Asp Asp Ser
 785 790 795 800
 Ile Lys Lys Ile Leu Glu Ser Ile Ser Glu Ser Lys Tyr His His Tyr
 805 810 815
 Leu Arg Leu Asn Pro Ser Gln Ser Ser Ser Leu Ile Lys Ser Glu Asn
 820 825 830
 Glu Glu Ile Gln Glu Leu Leu Lys
 835 840

(2) INFORMATION FOR SEQ ID NO:227:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

Gly Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr
 1 5 10 15
 Asp Ser Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys
 20 25 30
 Leu Leu

(2) INFORMATION FOR SEQ ID NO:228:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

Lys	Phe	Tyr	Lys	Gln	Thr	Lys	Gly	Ile	Pro	Gln	Gly	Leu	Cys	Val	Ser
1					5					10				15	
Ser	Ile	Leu	Ser	Ser	Phe	Tyr	Tyr	Ala	Thr	Leu	Glu	Glu	Ser	Ser	Leu
					20				25				30		
Gly	Phe	Leu													
		35													

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

Leu	Met	Arg	Leu	Thr	Asp	Asp	Tyr	Leu	Leu	Ile	Thr	Thr	Gln	Glu	Asn
1					5					10				15	
Asn	Ala	Val	Leu	Phe	Ile	Glu	Lys	Leu	Ile	Asn	Val	Ser	Arg	Glu	Asn
					20				25				30		
Gly	Phe	Lys	Phe	Asn	Met	Lys	Lys	Leu	Gln	Thr					
		35						40							

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

Gln	Asp	Tyr	Cys	Asp	Trp	Ile	Gly	Ile	Ser	Ile					
1					5				10						

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

Lys Asn Arg Asn Leu His Cys Thr Tyr Ile Asp Tyr Lys Lys Ala Phe
1 5 10 15

Asp Ser Ile Pro His Ser Trp Leu Ile Gln Val Leu Glu Ile Tyr Lys
20 25 30

Ile Asn

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

Arg Gln Ile Ala Ile Lys Lys Gly Ile Tyr Gln Gly Asp Ser Leu Ser
1 5 10 15

Pro Leu Trp Phe Cys Leu Ala Leu Asn Pro Leu Ser His Gln Leu His
20 25 30

Asn Asp Arg
35

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

His Leu Ile Tyr Met Asp Asp Ile Lys Leu Tyr Ala Lys Asn Asp Lys
1 5 10 15

Glu Met Lys Lys Leu Ile Asp Thr Thr Thr Ile Phe Ser Asn Asp Ile
20 25 30

Ser Met Gln Phe Gly Leu Asp Lys Cys Lys Thr
35 40

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

Lys Cys Leu Tyr Lys Tyr Leu Gly Phe Gln Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

Phe Gly Gly Ser Asn Trp Phe Arg Glu Val Asp Leu Lys Lys Cys Phe
1 5 10 15

Asp Thr Ile Ser His Asp Leu Ile Ile Lys Glu Leu Lys Arg Tyr Ile
20 25 30

Ser Asp

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

His Val Pro Val Gly Pro Arg Val Cys Val Gln Gly Ala Pro Thr Ser
1 5 10 15

Pro Ala Leu Cys Asn Ala Val Leu Leu Arg Leu Asp Arg Arg Leu Ala
20 25 30

Gly Leu Ala
35

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

Tyr Val Arg Tyr Ala Asp Asp Ile Leu Ile Gly Val Leu Gly Ser Lys
1 5 10 15

Asn

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

Lys Ile Ile Lys Arg Asp Leu Asn Asn Phe Leu Asn Ser Leu Gly Leu
1 5 10 15

Thr Ile Asn Glu Glu Lys Thr Leu Ile
20 25

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

Glu Thr Pro Ala Arg Phe Leu Gly Tyr Asn Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

Leu Lys Lys Lys Lys Ser Val Thr Val Leu Asp Val Gly Asp Ala Tyr
1 5 10 15

Phe Ser Val Pro Leu Asp Glu Asp Phe Arg Lys Tyr Thr Ala Phe Thr
20 25 30

Ile Pro

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

Gly Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser
1 5 10 15

Pro Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg
20 25 30

Lys Gln Asn
35

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser His Leu Glu Ile
1 5 10 15

Gly

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

His Arg Thr Lys Ile Glu Glu Leu Arg Gln His Leu Leu Arg Trp Gly
1 5 10 15

Leu Thr Thr Pro Asp Lys Lys His Gln Lys Glu Pro Pro Phe Leu Trp
20 25 30

Met Gly Tyr Glu Leu
35

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

Val Leu Pro Glu Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr
1 5 10 15

Asp Ser Ile Pro Arg Met Glu Cys Met Arg Ile Leu Lys Asp Ala Leu
20 25 30

Lys Asn

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

Lys	Cys	Tyr	Ile	Arg	Glu	Asp	Gly	Leu	Phe	Gln	Gly	Ser	Ser	Leu	Ser
1					5					10					15
Ala	Pro	Ile	Val	Asp	Leu	Val	Tyr	Asp	Asp	Leu	Leu	Glu	Phe	Tyr	Ser
					20				25					30	
Glu	Phe	Lys													
		35													

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

Ile	Leu	Lys	Leu	Ala	Asp	Asp	Phe	Leu	Ile	Ile	Ser	Thr	Asp	Gln	Gln
1					5					10					15
Gln	Val	Ile	Asn	Ile	Lys	Lys	Leu	Ala	Met	Gly	Gly	Phe	Gln	Lys	Tyr
					20				25					30	
Asn	Ala	Lys	Ala	Asn	Arg										
		35													

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

Ile	Arg	Ser	Lys	Ser	Ser	Lys	Gly	Ile	Phe	Arg
1				5					10	

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 1
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 4
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 6
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 10
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 13
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

Xaa Xaa Xaa Xaa Xaa Xaa Gln Gly Xaa Xaa Xaa Ser Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 8..10
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

Xaa Xaa Xaa Tyr Xaa Asp Asp Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 2
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 4
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

Gly Xaa Xaa Xaa Xaa Xaa Xaa Lys
1 5

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 1
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 3
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 6
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 8
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

Xaa Xaa Xaa Leu Gly Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

Tyr Tyr Tyr Arg Lys
1 5

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

Gly Lys Leu Arg Ile Ile Pro Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

Phe Arg Pro Ile Met Thr Phe
1 5

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe
1 5 10 15
Tyr Arg Lys Ser Val Trp Ser Lys
20

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

Arg Gln His Leu Lys Arg Val Gln Leu Arg Asp Val Ser Glu Ala Glu
1 5 10 15
Val Arg Gln His Arg Glu Ala
20

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

Ala	Arg	Thr	Phe	Arg	Arg	Glu	Lys	Arg	Ala	Glu	Arg	Leu	Thr	Ser	Arg
1				5					10					15	
Val	Lys	Ala	Leu	Phe	Ser	Val	Leu	Asn	Tyr	Glu					
			20				25								

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

Ala	Lys	Phe	Leu	His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu
1				5				10					15		
Arg	Ser	Phe	Phe	Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln				
			20			25									

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

Leu	Phe	Phe	Tyr	Arg	Lys	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly
1				5				10					15		
Ile	Arg	Gln	His	Leu	Lys	Arg	Val	Gln	Leu	Arg	Asp	Val	Ser		
			20			25						30			

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu	Arg	Phe	Ile	Pro	Lys	Pro	Asp	Gly
1															15
Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val															
20 25															

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

YARACHAARG GHATYCCHYA RGG

23

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

NGTNATDARD ARRTARTCRT C

21

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

Gln Thr Lys Gly Ile Pro Gln Gly
1 5

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

Asp Asp Tyr Leu Leu Ile Thr
1 5

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

Lys Gly Ile Pro Gln Gly Leu Cys Val Ser Ser Ile Leu Ser Ser Phe
1 5 10 15
Tyr Tyr Ala Thr Leu Glu Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu
20 25 30
Ser Met Asn Pro Glu Asn Pro Asn Val Asn Leu Leu Met Arg Leu Thr
35 40 45
Asp Asp Tyr Leu Leu Ile Thr
50 55

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

Ser Ile Leu Ser Ser Phe Leu Cys His Phe Tyr Met Glu Asp Leu Ile
1 5 10 15
Asp Glu Tyr Leu Ser Phe Thr Lys Lys Lys Gly Ser Val Leu Leu Arg
20 25 30
Val Val

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro Ile Val Asp Leu
1 5 10 15
Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser Glu Phe Lys Ala Ser Pro
20 25 30
Ser Gln Asp Thr Leu Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile
35 40 45
Ser

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

Gln Lys Val Gly Ile Pro Gln Gly
1 5

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

CAAAAAGTTG GTATCCCTCA GGG

23

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

AGACCAAAGG AATTCCATCA GGCTCAATTC TGTCATCTTT TTTGTGTCAT TTCTATATGG 60
AAGATTTGAT TGATGAATAC CTATCGTTA CGAAAAAGAA AGGATCAGTG TTGTTACGAG 120
TAGTCGACGA CTACCTCCTC ATCACCC 146

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

Lys	Gly	Ile	Pro	Ser	Gly	Ser	Ile	Leu	Ser	Ser	Phe	Leu	Cys	His	Phe
1				5					10					15	
Tyr	Met	Glu	Asp	Leu	Ile	Asp	Glu	Tyr	Leu	Ser	Phe	Thr	Lys	Lys	Lys
				20				25					30		
Gly	Ser	Val	Leu	Leu	Arg	Val	Val	Asp	Asp	Tyr	Leu	Leu	Ile	Thr	
				35			40						45		

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

GACGATTGCC TCTTTATAAC A

21

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

Asp Asp Phe Leu Phe Ile Thr
1 5

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

Trp Leu Tyr Asn Ser Phe Ile Ile Pro Ile Leu Gln Ser Phe Phe Tyr
1 5 10 15
Ile Thr Glu Ser Ser Asp Leu Arg Asn Arg Thr Val Tyr Phe Arg Lys
20 25 30
Asp Ile Trp
35

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

Ala Val Ile Arg Leu Leu Pro Lys Lys Asn Thr Phe Arg Leu Ile Thr
1 5 10 15

Asn Leu Arg Lys Arg Phe
20

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys Ser Cys Tyr Asp Arg Ile
1 5 10 15

Lys Gln Asp Leu Met Phe Arg Ile Val Lys
20 25

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile Leu Ser Ser Phe
1 5 10 15

Leu Cys His Phe Tyr Met Glu Asp Leu Ile Asp Glu Tyr Leu Ser Phe
20 25 30

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

Val Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile Thr Val Asn Lys
1 5 10 15

Lys Asp Ala Lys Lys Phe Leu Asn Leu Ser Leu Arg Gly Phe Glu Lys
20 25 30

His Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile Asn Phe Glu Asn
35 40 45

Ser

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

Trp Leu Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr
1 5 10 15

Cys Thr Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp
20 25 30

Thr Trp

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn Asn Glu Phe Arg Ile
1 5 10 15

Ile Ala Ile Pro Cys Arg Gly Ala Asp
20 25

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

Glu	Leu	Tyr	Phe	Met	Lys	Phe	Asp	Val	Lys	Ser	Cys	Tyr	Asp	Ser	Ile
1				5					10					15	
Pro	Arg	Met	Glu	Cys	Met	Arg	Ile	Leu	Lys						
			20						25						

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

Tyr	Ile	Arg	Glu	Asp	Gly	Leu	Phe	Gln	Gly	Ser	Ser	Leu	Ser	Ala	Pro
1				5				10						15	
Ile	Val	Asp	Leu	Val	Tyr	Asp	Asp	Leu	Leu	Glu	Phe	Tyr	Ser	Glu	Phe
				20				25					30		

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

Leu	Ile	Leu	Lys	Leu	Ala	Asp	Asp	Phe	Leu	Ile	Ile	Ser	Thr	Asp	Gln
1				5					10					15	
Gln	Gln	Val	Ile	Asn	Ile	Lys	Lys	Leu	Ala	Met	Gly	Gly	Phe	Gln	Lys
			20					25					30		
Tyr	Asn	Ala	Lys	Ala	Asn	Arg	Asp	Lys	Ile	Leu	Ala	Val	Ser	Ser	Gln
			35					40					45		
Ser															

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

Trp Ile Phe Glu Asp Leu Val Val Ser Leu Ile Arg Cys Phe Phe Tyr
1 5 10 15
Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys
20 25 30
Asn Ile Trp
35

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

Gly Lys Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met
1 5 10 15
Thr Phe Asn Lys Lys Ile Val
20

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp Ser Val
1 5 10 15
Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys
20 25

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

Tyr	Lys	Gln	Thr	Lys	Gly	Ile	Pro	Gln	Gly	Leu	Cys	Val	Ser	Ser	Ile
1				5						10					15
Leu	Ser	Ser	Phe	Tyr	Tyr	Ala	Thr	Leu	Glu	Glu	Ser	Ser	Leu	Gly	Phe
	20							25						30	

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

Leu	Leu	Met	Arg	Leu	Thr	Asp	Asp	Tyr	Leu	Leu	Ile	Thr	Thr	Gln	Glu
1				5					10						15
Asn	Asn	Ala	Val	Leu	Phe	Ile	Glu	Lys	Leu	Ile	Asn	Val	Ser	Arg	Glu
	20							25						30	
Asn	Gly	Phe	Lys	Phe	Asn	Met	Lys	Lys	Leu	Gln	Thr	Ser	Phe	Pro	Leu
	35						40							45	
Ser															

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 1
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

Xaa Pro Gln Gly
1

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 3
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 4
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 5
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

Asp Asp Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

Leu	Val	Val	Ser	Leu	Ile	Arg	Cys	Phe	Phe	Tyr	Val	Thr	Glu	Gln	Gln
1				5						10					15
Lys	Ser	Tyr	Ser	Lys	Thr										
				20											

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

Lys	Ser	Leu	Gly	Phe	Ala	Pro	Gly	Lys	Leu	Arg	Leu	Ile	Pro	Lys	Lys
1				5					10						15
Thr	Thr	Phe	Arg	Pro	Ile	Met	Thr	Phe	Asn	Lys	Lys	Ile	Val		
				20					25				30		

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

Pro	Lys	Leu	Phe	Phe	Ala	Thr	Met	Asp	Ile	Glu	Lys	Cys	Tyr	Asp	Ser
1				5					10						15
Val	Asn	Arg	Glu	Lys	Leu	Ser	Thr	Phe	Leu	Lys					
				20					25						

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

Asn	Gly	Lys	Phe	Tyr	Lys	Gln	Thr	Lys	Gly	Ile	Pro	Gln	Gly	Leu	Cys
1				5					10						15
Val	Ser	Ser	Ile	Leu	Ser	Ser	Phe	Tyr	Tyr	Ala					
			20					25							

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

Pro	Asn	Val	Asn	Leu	Leu	Met	Arg	Leu	Thr	Asp	Asp	Tyr	Leu	Leu	Ile
1				5					10						15
Thr	Thr	Gln	Glu	Asn	Asn										
		20													

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

Asn	Val	Ser	Arg	Glu	Asn	Gly	Phe	Lys	Phe	Asn	Met	Lys	Lys	Leu
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

Phe	Ile	Ile	Pro	Ile	Leu	Gln	Ser	Phe	Phe	Tyr	Ile	Thr	Glu	Ser	Ser
1				5					10				15		
Asp	Leu	Arg	Asn	Arg	Thr										
			20												

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

Gln	Lys	Thr	Thr	Leu	Pro	Pro	Ala	Val	Ile	Arg	Leu	Leu	Pro	Lys	Lys
1				5					10				15		
Asn	Thr	Phe	Arg	Leu	Ile	Thr	Asn	Leu	Arg	Lys	Arg	Phe	Leu		
		20						25				30			

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

Arg	Lys	Lys	Tyr	Phe	Val	Arg	Ile	Asp	Ile	Lys	Ser	Cys	Tyr	Asp	Arg
1				5					10				15		
Ile	Lys	Gln	Asp	Leu	Met	Phe	Arg	Ile	Val	Lys					
			20						25						

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

Gly	Asn	Ser	Gln	Tyr	Leu	Gln	Lys	Val	Gly	Ile	Pro	Gln	Gly	Ser	Ile
1				5					10						15
Leu	Ser	Ser	Phe	Leu	Cys	His	Phe	Tyr	Met	Glu					
			20					25							

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

Lys	Lys	Gly	Ser	Val	Leu	Leu	Arg	Val	Val	Asp	Asp	Phe	Leu	Phe	Ile
1				5					10						15
Thr	Val	Asn	Lys	Lys	Asp										
			20												

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

Leu	Asn	Leu	Ser	Leu	Arg	Gly	Phe	Glu	Lys	His	Asn	Phe	Ser	Thr
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

Leu	Ile	Pro	Lys	Ile	Ile	Gln	Thr	Phe	Phe	Tyr	Cys	Thr	Glu	Ile	Ser	
1					5									10		15
Ser	Thr	Val	Thr	Ile	Val											
				20												

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

Thr	Leu	Ser	Asn	Phe	Asn	His	Ser	Lys	Met	Arg	Ile	Ile	Pro	Lys	Lys	
1					5						10			15		
Ser	Asn	Asn	Glu	Phe	Arg	Ile	Ile	Ala	Ile	Pro	Cys	Arg	Gly	Ala	Asp	
			20						25					30		

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

Pro	Glu	Leu	Tyr	Phe	Met	Lys	Phe	Asp	Val	Lys	Ser	Cys	Tyr	Asp	Ser	
1					5					10			15			
Ile	Pro	Arg	Met	Glu	Cys	Met	Arg	Ile	Leu	Lys						
			20						25							

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

Glu	Asp	Lys	Cys	Tyr	Ile	Arg	Glu	Asp	Gly	Leu	Phe	Gln	Gly	Ser	Ser
1					5					10					15
Leu	Ser	Ala	Pro	Ile	Val	Asp	Leu	Val	Tyr	Asp					
					20			25							

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

Ser	Gln	Asp	Thr	Leu	Ile	Leu	Lys	Leu	Ala	Asp	Asp	Phe	Leu	Ile	Ile
1					5					10					15
Ser	Thr	Asp	Gln	Gln	Gln										
				20											

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

Lys	Lys	Leu	Ala	Met	Gly	Gly	Phe	Gln	Lys	Tyr	Asn	Ala	Lys	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr
1 5 10 15

Phe Gln Lys Asn Arg Leu
20

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
1 5 10 15

Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly
20 25 30

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr
1 5 10 15

Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala
20 25

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

Arg	Ala	Thr	Ser	Tyr	Val	Gln	Cys	Gln	Gly	Ile	Pro	Gln	Gly	Ser	Ile
1				5						10				15	
Leu	Ser	Thr	Leu	Leu	Cys	Ser	Leu	Cys	Tyr	Gly					
			20						25						

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

Arg	Arg	Asp	Gly	Leu	Leu	Leu	Arg	Leu	Val	Asp	Asp	Phe	Leu	Leu	Val
1				5					10				15		
Thr	Pro	His	Leu	Thr	His										
			20												

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro	Glu	Tyr	Gly	Cys	Val	Val
1				5					10				15	

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 261 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

Ala Ala Leu Arg Pro Ala Ala His Val Gly Ser Pro Gly Pro Gly His
1 5 10 15

Pro Arg Asp Ala Ala Arg Ser Pro Leu Pro Ser Arg Ala Leu Pro Ala
20 25 30

Ala Gln Pro Leu Pro Arg Gly Ala Ala Ala Gly His Val Arg Ala Ala
35 40 45

Pro Gly Ala Pro Gly Leu Ala Ala Gly Ala Ala Arg Gly Pro Gly Gly
50 55 60

Phe Pro Arg Xaa Gly Gly Pro Xaa Xaa Gly Val Arg Ala Leu Gly Xaa
65 70 75 80

Xaa Ala Ala Pro Arg Arg Pro Leu Leu Pro Pro Gly Val Leu Pro Glu
85 90 95

Xaa Xaa Gly Gly Pro Ser Ala Ala Xaa Ala Val Arg Xaa Arg Arg Glu
100 105 110

Xaa Arg Ala Gly Leu Arg Leu Arg Ala Ala Gly Arg Gly Pro Arg Gly
115 120 125

Pro Pro Arg Gly Leu His His Gln Arg Ala Gln Leu Pro Ala Gln His
130 135 140

Gly Asp Arg Arg Thr Ala Gly Glu Arg Gly Val Gly Ala Ala Ala Ala
145 150 155 160

Pro Arg Gly Arg Arg Ala Gly Ser Pro Ala Gly Thr Leu Arg Xaa
165 170 175

Xaa Cys Ala Gly Gly Ser Gln Leu Arg Leu Pro Xaa Val Arg Ala Ala
180 185 190

Ala Val Pro Ala Arg Arg Cys Xaa Ser Gly Pro Ala Pro Ala Thr Arg
195 200 205

Xaa Trp Thr Arg Xaa Arg Leu Gly Ser Asn Gly Pro Gly Thr Ile Ala
210 215 220

Ser Gly Arg Pro Gly Ser Pro Trp Ala Ala Ser Pro Gly Cys Glu Glu
225 230 235 240

Ala Arg Gly Gln Cys Gln Pro Lys Ser Ala Val Ala Gln Glu Ala Gln
245 250 255

Ala Trp Arg Cys Pro
260

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

Ala Gly Ala Asp Ala Arg Trp Ala Gly Val Leu Gly Pro Pro Gly Gln
1 5 10 15
Asp Ala Trp Thr Glu
20

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

Pro Trp Phe Leu Cys Gly Val Thr Cys Gln Thr Arg Arg Arg Ser His
1 5 10 15
Leu Phe Gly Gly Cys Ala Leu Trp His Ala Pro Leu Pro Pro Ile Arg
20 25 30
Gly Pro Pro Ala Pro Arg Gly Pro Pro Ile His Ile Ala Ala Thr Thr
35 40 45
Ser Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe
50 55 60
Leu Tyr Ser Ser Gly Asp Lys Xaa Thr Ala Xaa Leu Leu Pro Thr Gln
65 70 75 80
Tyr Ile

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

Leu Ala Phe Gly Arg Phe Val Glu Thr Xaa Phe Leu Val Pro Gly Leu
1 5 10 15

Gly Cys Gln Asp Ser Pro Gln Val Ala Pro Pro Ala Pro Ala Xaa Leu
20 25 30

Ala Asn Ala Ala Pro Val Ser Gly Ala Ala Trp Glu Pro Arg Ala Val
35 40 45

Pro Leu Arg Gly Val Pro Gln Asp Ala Leu Pro Ala Ala Ser Cys Gly
50 55 60

His Pro Ser Ser Arg Cys Leu Cys Pro Gly Glu Ala Pro Gly Leu Cys
65 70 75 80

Gly Gly Pro Arg Gly Gly Thr Gln Thr Pro Val Ala Trp Cys Ser
85 90 95

Cys Ser Ala Ser Thr Ala Ala Pro Gly Arg Cys Thr Ala Ser Cys Gly
100 105 110

Pro Ala Cys Ala Gly Trp Cys Pro Gln Ala Ser Gly Ala Pro Gly Thr
115 120 125

Thr Asn Ala Ala Ser Ser Gly Thr Pro Arg Ser Ser Ser Pro Trp Gly
130 135 140

Ser Met Pro Ser Ser Arg Cys Arg Ser
145 150

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

Ala Cys Gly Thr Ala Leu Gly Cys Ala Gly Ala Gln Gly Leu Ala Val
1 5 10 15

Phe Arg Pro Gln Ser Thr Val Cys Val Arg Arg Ser Trp Pro Ser Ser
20 25 30

Cys Thr Gly
35

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

Val Cys Thr Ser Ser Cys Ser Gly Leu Ser Phe Met Ser Arg Arg
1 5 10 15

Pro Arg Phe Lys Arg Thr Gly Ser Phe Ser Thr Gly Arg Val Ser Gly
20 25 30

Ala Ser Cys Lys Ala Leu Glu Ser Asp Ser Thr
35 40

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

Arg Gly Cys Ser Cys Gly Ser Cys Arg Lys Gln Arg Ser Gly Ser Ile
1 5 10 15

Gly Lys Pro Gly Pro Pro Cys
20

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

Arg Pro Asp Ser Ala Ser Ser Pro Ser Leu Thr Gly Cys Gly Arg Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

Thr Trp Thr Thr Ser Trp Glu Pro Glu Arg Ser Ala Glu Lys Arg Gly
1 5 10 15
Pro Ser Val Ser Pro Arg Gly
20

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

Arg His Cys Ser Ala Cys Ser Thr Thr Ser Gly Arg Gly Ala Pro Ala
1 5 10 15
Ser Trp Ala Pro Leu Cys Trp Ala Trp Thr Ile Ser Thr Gly Pro Gly
20 25 30
Ala Pro Ser Cys Cys Val Cys Gly Pro Arg Thr Arg Arg Leu Ser Cys
35 40 45
Thr Leu Ser Arg Trp Met
50

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

Arg Ala Arg Thr Thr Pro Ser Pro Arg Thr Gly Ser Arg Arg Ser Ser
1 5 10 15

Pro Ala Ser Ser Asn Pro Arg Thr Arg Thr Ala Cys Val Gly Met Pro
20 25 30

Trp Ser Arg Arg Pro Pro Met Gly Thr Ser Ala Arg Pro Ser Arg Ala
35 40 45

Thr Ser Leu Pro
50

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

Gln Thr Ser Ser Arg Thr Cys Asp Ser Ser Trp Leu Thr Cys Arg Xaa
1 5 10 15

Thr Ala Arg

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

Gly Met Pro Ser Ser Ser Ser Arg Ala Pro Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

Met Arg Pro Ala Val Ala Ser Ser Thr Ser Ser Tyr Ala Ser Cys Ala
1 5 10 15

Thr Thr Pro Cys Ala Ser Gly Ala Ser Pro Thr Ser Ser Ala Arg Gly
20 25 30

Ser Arg Arg Ala Pro Ser Ser Pro Arg Cys Ser Ala Ala Cys Ala Thr
35 40 45

Ala Thr Trp Arg Thr Ser Cys Leu Arg Gly Phe Gly Gly Thr Gly Cys
50 55 60

Ser Cys Val Trp Trp Met Ile Ser Cys Trp
65 70

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

His Leu Thr Ser Pro Thr Arg Lys Pro Ser Ser Gly Pro Trp Ser Glu
1 5 10 15

Val Ser Leu Ser Met Ala Ala Trp
20

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

Thr Cys Gly Arg Gln Trp
1 5

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

Lys Thr Arg Pro Trp Val Ala Arg Leu Leu Phe Arg Cys Arg Pro Thr
1 5 10 15

Ala Tyr Ser Pro Gly Ala Ala Cys Cys Trp Ile Pro Gly Pro Trp Arg
20 25 30

Cys Arg Ala Thr Thr Pro Ala Met Pro Gly Pro Pro Ser Glu Pro Val
35 40 45

Ser Pro Ser Thr Ala Ala Ser Arg Leu Gly Gly Thr Cys Val Ala Asn
50 55 60

Ser Leu Gly Ser Cys Gly
65 70

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

Ser Val Thr Ala Cys Phe Trp Ile Cys Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

Thr Ala Ser Arg Arg Cys Ala Pro Thr Ser Thr Arg Ser Ser Cys Cys
1 5 10 15

Arg Arg Thr Gly Phe Thr His Val Cys Cys Ser Ser His Phe Ile Ser
20 25 30

Lys Phe Gly Arg Thr Pro His Phe Ser Cys Ala Ser Ser Leu Thr Arg
35 40 45

Pro Pro Ser Ala Thr Pro Ser
50 55

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

Lys Pro Arg Thr Gln Gly Cys Arg Trp Gly Pro Arg Ala Pro Pro Ala
1 5 10 15

Leu Cys Pro Pro Arg Pro Cys Ser Gly Cys Ala Thr Lys His Ser Cys
20 25 30

Ser Ser

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

Leu Asp Thr Val Ser Pro Thr Cys His Ser Trp Gly His Ser Gly Gln
1 5 10 15

Pro Arg Arg Ser
20

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

Val Gly Ser Ser Arg Gly Arg Arg
1 5

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

Leu Pro Trp Arg Pro Gln Pro Thr Arg His Cys Pro Gln Thr Ser Arg
1 5 10 15
Pro Ser Trp Thr Asp Gly His Pro Pro Thr Ala Arg Pro Arg Ala Asp
20 25 30
Thr Ser Ser Pro Val Thr Pro Gly Ser Thr Ser Gln Gly Gly Arg Gly
35 40 45
Gly Pro His Pro Gly Pro His Arg Trp Glu Ser Glu Ala
50 55 60

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

Val Ser Val Trp Pro Arg Pro Ala Cys Pro Ala Glu Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

Gly Leu Ser Glu Cys Pro Ala Lys Gly
1 5

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

Val Ser Ser Thr Pro Ala Val Phe Thr Ser Pro Gln Ala Gly Ala Arg
1 5 10 15

Leu His Pro Arg Ala Ser Phe Ser Ser Pro Gly Ala Arg Leu Pro Leu
20 25 30

Pro Thr

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

Ser Ile Pro Arg Phe Ala Ile Val His Pro Ser Pro Cys Pro Pro Leu
1 5 10 15

Pro Ser Thr Pro Thr Ile Gln Val Glu Thr Leu Arg Arg Thr Leu Gly
20 25 30

Ala Leu Gly Ile Trp Ser Asp Gln Arg Cys Ala Leu Tyr Thr Gly Glu
35 40 45

Asp Pro Ala Pro Gly Trp Gly Ser Leu Trp Val Lys Leu Gly Gly Gly
50 55 60

Ala Val Gly Val Lys Tyr
65 70

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

Ile Tyr Glu Phe Phe Ser Phe Glu Lys Lys Lys Lys Lys Lys Lys Lys Lys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

Gln Arg Cys Val Leu Leu Arg Thr Trp Glu Ala Leu Ala Pro Ala Thr
1 5 10 15

Pro Ala Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu
20 25 30

Arg Ser His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg
35 40 45

Leu Gly Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala
50 55 60

Phe Arg Ala Xaa Val Ala Xaa Cys Xaa Val Cys Val Pro Trp Xaa Xaa
65 70 75 80

Xaa Xaa Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Xaa
85 90 95

Xaa Leu Val Ala Arg Val Leu Xaa Xaa Leu Cys Xaa Arg Gly Ala Xaa
100 105 110

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
115 120 125

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
130 135 140

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
145 150 155 160

Arg	Val	Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Xaa
					165				170						175
Phe	Val	Leu	Val	Xaa	Pro	Ser	Cys	Ala	Tyr	Xaa	Val	Cys	Gly	Pro	Pro
					180				185						190
Leu	Tyr	Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala
					195			200							205
Xaa	Gly	Pro	Glu	Xaa	Val	Trp	Asp	Pro	Thr	Gly	Leu	Glu	Pro		
					210		215			220					

(2) INFORMATION FOR SEQ ID NO:345:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 330 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

Arg	Gln	Gly	Gly	Arg	Gly	Pro	Pro	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg
1				5					10						15
Arg	Arg	Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro
				20			25						30		
Arg	Arg	Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly
				35		40							45		
Ser	Trp	Ala	His	Pro	Gly	Arg	Thr	Pro	Gly	Pro	Ser	Asp	Arg	Gly	Phe
				50		55							60		
Cys	Val	Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu
					65		70		75						80
Gly	Ala	Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln
					85			90						95	
His	His	Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Gly	Thr
					100			105							110
Arg	Leu	Val	Pro	Arg	Cys	Thr	Pro	Arg	Pro	Ser	Thr	Ser	Ser	Thr	Pro
					115		120								125
Gln	Ala	Thr	Xaa	Thr	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Asn	Ile	Ser	Glu
					130		135								140
Ala	Gln	Pro	Asp	Trp	Arg	Ser	Gly	Gly	Ser	Trp	Arg	Xaa	Ser	Phe	Trp
					145		150			155					160
Phe	Gln	Ala	Leu	Asp	Ala	Arg	Ile	Pro	Arg	Arg	Leu	Pro	Arg	Leu	Pro
						165			170						175
Gln	Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Gly	Asn	
					180			185							190

His	Ala	Gln	Cys	Pro	Tyr	Gly	Val	Phe	Leu	Lys	Thr	His	Cys	Pro	Leu
195							200				205				
Arg	Ala	Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys	Pro
210							215			220					
Gln	Gly	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	His	Arg	Pro	Pro	Ser	
225							230		235			240			
Pro	Gly	Ala	Ala	Ala	Pro	Pro	Ala	Gln	Gln	Pro	Leu	Ala	Gly	Val	Arg
							245		250			255			
Leu	Arg	Ala	Gly	Leu	Pro	Ala	Pro	Ala	Gly	Ala	Pro	Arg	Pro	Leu	Gly
							260		265			270			
Leu	Gln	Ala	Gln	Arg	Thr	Pro	Leu	Pro	Gln	Glu	His	Gln	Glu	Val	His
							275		280			285			
Leu	Pro	Gly	Glu	Ala	Cys	Gln	Ala	Leu	Ala	Ala	Gly	Ala	Asp	Val	Glu
							290		295			300			
Asp	Glu	Arg	Ala	Gly	Leu	Arg	Leu	Ala	Ala	Gln	Glu	Pro	Arg	Gly	Trp
							305		310			315			320
Leu	Cys	Ser	Gly	Arg	Arg	Ala	Pro	Ser	Ala						
							325		330						

(2) INFORMATION FOR SEQ ID NO:346:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

Gly	Asp	Pro	Gly	Gln	Val	Pro	Ala	Leu	Ala	Asp	Glu	Cys	Val	Arg	Arg
1					5								10		15
Arg	Ala	Ala	Gln	Val	Phe	Leu	Leu	Cys	His	Gly	Asp	His	Val	Ser	Lys
													20	25	30
Glu	Gln	Ala	Leu	Phe	Leu	Pro	Glu	Glu	Cys	Leu	Glu	Gln	Val	Ala	Lys
												35	40	45	
His	Trp	Asn	Gln	Thr	Ala	Leu	Glu	Glu	Gly	Ala	Ala	Gly	Ala	Val	
												50	55	60	
Gly	Ser	Arg	Gly	Gln	Ala	Ala	Ser	Gly	Ser	Gln	Ala	Arg	Pro	Ala	Asp
												65	70	75	80
Val	Gln	Thr	Pro	Leu	His	Pro	Gln	Ala							
							85								

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

Arg Ala Ala Ala Asp Cys Glu His Gly Leu Arg Arg Gly Ser Gln Asn
1 5 10 15

Val Pro Gln Arg Lys Glu Gly Arg Ala Ser His Leu Glu Gly Glu Gly
20 25 30

Thr Val Gln Arg Ala Gln Leu Arg Ala Gly Ala Ala Pro Arg Pro Pro
35 40 45

Gly Arg Leu Cys Ala Gly Pro Gly Arg Tyr Pro Gln Gly Leu Ala His
50 55 60

Leu Arg Ala Ala Cys Ala Gly Pro Gly Pro Ala Ala
65 70 75

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

Ala Val Leu Cys Gln Gly Gly Cys Asp Gly Arg Val Arg His His Pro
1 5 10 15

Pro Gly Gln Ala His Gly Gly His Arg Gln His His Gln Thr Pro Glu
20 25 30

His Val Leu Arg Ala Ser Val Cys Arg Gly Pro Glu Gly Arg Pro Trp
35 40 45

Ala Arg Pro Gln Gly Leu Gln Glu Pro Arg Leu Tyr Leu Asp Arg Pro
50 55 60

Pro Ala Val His Ala Thr Val Arg Gly Ser Pro Ala Gly Xaa Gln Pro
65 70 75 80

Ala Glu Gly Cys Arg Arg His Arg Ala Glu Leu Leu Pro Glu
85 90

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

Gly Gln Gln Trp Pro Leu Arg Arg Leu Pro Thr Leu His Val Pro Pro
1 5 10 15

Arg Arg Ala His Gln Gly Gln Val Leu Arg Pro Val Pro Gly Asp Pro
20 25 30

Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val Leu Arg Arg
35 40 45

His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg Ala Ala Pro
50 55 60

Ala Phe Gly Gly
65

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

Phe Leu Val Gly Asp Thr Ser Pro His Pro Arg Glu Asn Leu Pro Gln
1 5 10 15

Asp Pro Gly Pro Arg Cys Pro
20

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

Val Trp Leu Arg Gly Glu Leu Ala Glu Asp Ser Gly Glu Leu Pro Cys
1 5 10 15

Arg Arg Arg Gly Pro Gly Trp His Gly Phe Cys Ser Asp Ala Gly Pro
20 25 30

Arg Pro Ile Pro Leu Val Arg Pro Ala Ala Gly Tyr Pro Asp Pro Gly
35 40 45

Gly Ala Glu Arg Leu Leu Gln Leu Cys Pro Asp Leu His Gln Ser Gln
50 55 60

Ser His Leu Gln Pro Arg Leu Gln Gly Trp Glu Glu His Ala Ser Gln
65 70 75 80

Thr Leu Trp Gly Leu Ala Ala Glu Val Ser Gln Pro Val Ser Gly Phe
85 90 95

Ala Gly Glu Gln Pro Pro Asp Gly Val His Gln His Leu Gln Asp Pro
100 105 110

Pro Ala Ala Gly Val Gln Val Ser Arg Met Cys Ala Ala Ala Pro Ile
115 120 125

Ser Ser Ala Ser Leu Glu Pro His Ile Phe Pro Ala Arg His Leu
130 135 140

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

His Gly Leu Pro Leu Leu His Pro Glu Ser Gln Glu Arg Arg Asp
1 5 10 15

Val Ala Gly Gly Gln Gly Arg Arg Pro Ser Ala Leu Arg Gly Arg
20 25 30

Ala Val Ala Val Pro Pro Ser Ile Pro Ala Gln Ala Asp Ser Thr Pro
35 40 45

Cys His Leu Arg Ala Thr Pro Gly Val Thr Gln Asp Ser Pro Asp Ala
50 55 60

Ala Glu Ser Glu Ala Pro Gly Asp Asp Ala Asp Cys Pro Gly Gly Arg
65 70 75 80

Ser Gln Pro Gly Thr Ala Leu Arg Leu Gln Asp His Pro Gly Leu Met
85 90 95

Ala Thr Arg Pro Gln Pro Gly Arg Glu Gln Thr Pro Ala Ala Leu Ser
100 105 110
Arg Arg Ala Leu Arg Pro Arg Glu Gly Gly Ala Ala His Thr Gln Ala
115 120 125
Arg Thr Ala Gly Ser Leu Arg Pro Glu
130 135

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

Val Phe Gly Arg Gly Leu His Val Arg Leu Lys Ala Glu Cys Pro Ala
1 5 10 15
Glu Ala

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

Ala Ser Val Gln Pro Arg Ala Glu Cys Pro Ala His Leu Pro Ser Ser
1 5 10 15
Leu Pro His Arg Leu Ala Leu Gly Ser Thr Pro Gly Pro Ala Phe Pro
20 25 30
His Gln Glu Pro Gly Phe His Ser Pro His Arg Asn Ser Pro Ser Pro
35 40 45
Asp Ser Pro Leu Phe Thr Pro Arg Pro Ala Leu Leu Cys Leu Pro Pro
50 55 60
Pro Pro Ser Arg Trp Arg Pro
65 70

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

Glu	Gly	Pro	Trp	Glu	Leu	Trp	Glu	Phe	Gly	Val	Thr	Lys	Gly	Val	Pro
1				5						10					15
Cys	Thr	Gln	Ala	Arg	Thr	Leu	His	Leu	Asp	Gly	Gly	Pro	Cys	Gly	Ser
					20				25					30	
Asn	Trp	Gly	Glu	Va	Leu	Trp	Glu								
				35				40							

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

Asn	Thr	Glu	Tyr	Met	Ser	Phe	Ser	Val	Leu	Lys	Lys	Lys	Lys	Lys	Lys
1				5					10					15	
Lys	Lys														

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

Ser	Ala	Ala	Ser	Cys	Cys	Ala	Arg	Gly	Lys	Pro	Trp	Pro	Arg	Pro	Pro
1				5					10					15	
Pro	Arg	Cys	Arg	Ala	Leu	Pro	Ala	Ala	Glu	Pro	Cys	Ala	Pro	Cys	Cys
					20				25				30		

Ala	Ala	Thr	Thr	Ala	Arg	Cys	Cys	Arg	Trp	Pro	Arg	Ser	Cys	Gly	Ala
35															45
Trp	Gly	Pro	Arg	Ala	Gly	Gly	Trp	Cys	Ser	Ala	Gly	Thr	Arg	Arg	Leu
50															60
Ser	Ala	Arg	Trp	Trp	Pro	Xaa	Ala	Trp	Cys	Ala	Cys	Pro	Gly	Xaa	Xaa
65															80
Gly	Xaa	Pro	Pro	Pro	Pro	Pro	Ser	Ala	Arg	Cys	Pro	Ala			
							85								90

(2) INFORMATION FOR SEQ ID NO:358:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

Xaa	Xaa	Trp	Trp	Pro	Glu	Cys	Cys	Xaa	Xaa	Cys	Ala	Xaa	Ala	Ala	Arg
1															15
Xaa	Thr	Cys	Trp	Pro	Ser	Ala	Ser	Arg	Cys	Trp	Thr	Gly	Pro	Ala	Gly
	20														30
Ala	Pro	Pro	Arg	Pro	Ser	Pro	Pro	Ala	Cys	Ala	Ala	Thr	Cys	Pro	Thr
	35														45
Arg															

(2) INFORMATION FOR SEQ ID NO:359:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1003 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

Pro	Thr	His	Cys	Gly	Gly	Ala	Gly	Arg	Gly	Gly	Cys	Cys	Cys	Ala	Ala
1															15
Trp	Ala	Thr	Thr	Cys	Trp	Phe	Thr	Cys	Trp	His	Ala	Ala	Arg	Xaa	Leu
															30
Cys	Trp	Trp	Xaa	Pro	Ala	Ala	Pro	Thr	Xaa	Cys	Ala	Gly	Arg	Arg	Cys
															45
35															

Thr Ser Ser Ala Leu Xaa Leu Arg Pro Gly Pro Arg His Thr Leu Xaa
 50 55 60

Asp Pro Xaa Ala Ser Gly Ile Gln Arg Ala Trp Asn His Ser Val Arg
 65 70 75 80

Glu Ala Gly Val Pro Leu Gly Cys Gln Pro Arg Val Arg Gly Gly Ala
 85 90 95

Gly Ala Val Pro Ala Glu Val Cys Arg Cys Pro Arg Gly Pro Gly Val
 100 105 110

Ala Leu Pro Leu Ser Arg Ser Gly Arg Pro Leu Gly Arg Gly Pro Gly
 115 120 125

Pro Thr Arg Ala Gly Arg Leu Asp Arg Val Thr Val Val Ser Val Trp
 130 135 140

Cys His Leu Pro Asp Pro Pro Lys Lys Pro Pro Leu Trp Arg Val Arg
 145 150 155 160

Ser Leu Ala Arg Ala Thr Pro Thr His Pro Trp Ala Ala Ser Thr Thr
 165 170 175

Arg Ala Pro His Pro His Arg Gly His His Val Leu Gly His Ala Leu
 180 185 190

Ser Pro Gly Val Arg Arg Asp Gln Ala Leu Pro Leu Leu Leu Arg Arg
 195 200 205

Gln Xaa His Cys Xaa Pro Pro Ser Tyr Ser Ile Tyr Leu Arg Pro Ser
 210 215 220

Leu Thr Gly Val Arg Glu Val Arg Gly Asp Xaa Leu Ser Gly Ser Arg
 225 230 235 240

Pro Trp Met Pro Gly Phe Pro Ala Gly Cys Pro Ala Cys Pro Ser Xaa
 245 250 255

Thr Gly Lys Cys Gly Pro Cys Phe Trp Ser Cys Leu Gly Thr Thr Arg
 260 265 270

Ser Ala Pro Thr Gly Cys Ser Ser Arg Arg Thr Ala Arg Cys Glu Leu
 275 280 285

Arg Ser Pro Gln Gln Pro Val Ser Val Pro Gly Arg Ser Pro Arg Ala
 290 295 300

Leu Trp Arg Pro Pro Arg Arg Asn Thr Asp Pro Arg Arg Leu Val
 305 310 315 320

Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val
 325 330 335

Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg
 340 345 350

His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu
 355 360 365

Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser
 370 375 380
 Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val
 385 390 395 400
 Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu
 405 410 415
 His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe
 420 425 430
 Tyr Val Thr Glu Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg
 435 440 445
 Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu
 450 455 460
 Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His
 465 470 475 480
 Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro
 485 490 495
 Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly
 500 505 510
 Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg
 515 520 525
 Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro
 530 535 540
 Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala
 545 550 555 560
 Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu
 565 570 575
 Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro
 580 585 590
 Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn
 595 600 605
 Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly
 610 615 620
 His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu
 625 630 635 640
 Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Xaa Asn Ser Pro
 645 650 655
 Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala
 660 665 670
 Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala
 675 680 685

Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln
 690 695 700
 Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met
 705 710 715 720
 Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg
 725 730 735
 Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys
 740 745 750
 Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val
 755 760 765
 Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala
 770 775 780
 Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro
 785 790 795 800
 Trp Cys Gly Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp
 805 810 815
 Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn
 820 825 830
 Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val
 835 840 845
 Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser
 850 855 860
 Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala
 865 870 875 880
 Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val
 885 890 895
 Trp Lys Asn Pro Thr Phe Leu Arg Val Ile Ser Asp Thr Ala Ser
 900 905 910
 Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly
 915 920 925
 Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu
 930 935 940
 Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr
 945 950 955 960
 Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg
 965 970 975
 Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Asn Pro
 980 985 990
 Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 995 1000

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

Trp	Pro	Pro	Ala	His	Ser	Gln	Ala	Glu	Ser	Arg	His	Gln	Gln	Pro	Cys
1				5					10					15	
His	Ala	Gly	Leu	Tyr	Val	Pro	Gly	Arg	Glu	Gly	Arg	Pro	Thr	Pro	Arg
			20					25					30		
Pro	Ala	Pro	Leu	Gly	Val										
			35												

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

Gly	Leu	Ser	Glu	Cys	Leu	Ala	Glu	Ala	Cys	Met	Ser	Gly		
1				5					10					

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

Arg	Leu	Ser	Val	Arg	Leu	Arg	Pro	Glu	Arg	Val	Ser	Ser	Gln	Gly	Leu
1				5					10				15		
Ser	Val	Gln	His	Thr	Cys	Arg	Leu	His	Phe	Pro	Thr	Gly	Trp	Arg	Ser
			20					25				30			
Ala	Pro	Pro	Gln	Gly	Gln	Leu	Phe	Leu	Thr	Arg	Ser	Pro	Ala	Ser	Thr
			35					40			45				

Pro His Ile Gly Ile Val His Pro Gln Ile Arg His Cys Ser Pro Leu
50 55 60

Ala Leu Pro Ser Phe Ala Phe His Pro His His Pro Gly Gly Asp Pro
65 70 75 80

Glu Lys Asp Pro Gly Ser Ser Gly Asn Leu Glu
85 90

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

Pro Lys Val Cys Pro Val His Arg Arg Gly Pro Cys Thr Trp Met Gly
1 5 10 15

Val Pro Val Gly Gln Ile Gly Gly Arg Cys Cys Gly Ser Lys Ile Leu
20 25 30

Asn Ile

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

Val Phe Gln Phe
1

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

Lys Lys Lys Lys Lys Lys Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid,
selected from Gly, Ser, Thr, Tyr, Cys,
Asn or Gln"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

Xaa Phe Phe Tyr
1

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

Xaa Arg Xaa Ile Pro Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 3
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

Phe Arg Xaa Ile
1

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 2
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = charged amino acid,
selected from Asp, Glu, His, Lys or Arg"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 6
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

Pro Xaa Leu Tyr Phe Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

Gly Ile Pro Gln Gly Ser
1 5

(2) INFORMATION FOR SEQ ID NO:371:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

Leu Leu Arg Leu
1

(2) INFORMATION FOR SEQ ID NO:372:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 5
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

Asp Asp Phe Leu Xaa Ile Thr
1 5

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

Trp Leu Tyr Asn Ser Phe Ile Ile Pro Ile Leu Gln Ser Phe Phe Tyr
1 5 10 15
Ile Thr Glu Ser Ser Asp Leu Arg Asn Arg Thr Val Tyr Phe Arg Lys
20 25 30
Asp Ile Trp Lys Leu Leu Cys Arg Pro Phe Ile Thr Ser Met Lys Met
35 40 45

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

Asn Asn Val Arg Met Asp Thr Gln Lys Thr Thr Leu Pro Pro Ala Val
1 5 10 15
Ile Arg Leu Leu Pro Lys Lys Asn Thr Phe Arg Leu Ile Thr Asn Leu
20 25 30
Arg Lys Arg Phe Leu Ile Lys Met Gly Ser Asn Lys Lys Met Leu Val
35 40 45
Ser Thr Asn Gln Thr Leu
50

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

Phe Gly Arg Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys Ser Cys Tyr
1 5 10 15

Asp Arg Ile Lys Gln Asp Leu Met Phe Arg Ile Val Lys Lys Lys Leu
20 25 30

Lys Asp

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

Ser Gln Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile Leu Ser
1 5 10 15

Ser Phe Leu Cys His Phe Tyr Met Glu Asp Leu Ile Asp Glu Tyr Leu
20 25 30

Ser Phe Thr
35

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile Thr Val Asn Lys Lys
1 5 10 15

Asp Ala Lys Lys Phe Leu Asn Leu Ser Leu Arg Gly Phe Glu Lys His
20 25 30

Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile
35 40

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

Lys Lys Arg Met Pro Phe Phe Gly Phe Ser Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:379:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr
1 5 10 15
Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys
20 25 30
Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys
35 40 45

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

Glu	Val	Arg	Gln	His	Arg	Glu	Ala	Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg
1				5					10				15		
Leu	Arg	Phe	Ile	Pro	Lys	Pro	Asp	Gly	Leu	Arg	Pro	Ile	Val	Asn	Met
			20					25				30			
Asp	Tyr	Val	Val	Gly	Ala	Arg	Thr	Phe	Arg	Arg	Glu	Lys	Arg	Ala	Glu
				35				40			45				
Arg	Leu	Thr	Ser	Arg	Val										
	50														

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

Pro	Pro	Pro	Glu	Leu	Tyr	Phe	Val	Lys	Val	Asp	Val	Thr	Gly	Ala	Tyr
1				5					10			15			
Asp	Thr	Ile	Pro	Gln	Asp	Arg	Leu	Thr	Glu	Val	Ile	Ala	Ser	Ile	Ile
			20					25			30				
Lys	Pro														

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

Lys	Ser	Tyr	Val	Gln	Cys	Gln	Gly	Ile	Pro	Gln	Gly	Ser	Ile	Leu	Ser
1					5					10		15			
Thr	Leu	Leu	Cys	Ser	Leu	Cys	Tyr	Gly	Asp	Met	Glu	Asn	Lys	Leu	Phe
			20					25			30				
Ala	Gly	Ile													
	35														

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr
1 5 10 15

His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr
20 25 30

Gly Cys Val Val Asn Leu Arg Lys Thr Val Val
35 40

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

Trp Ile Phe Glu Asp Leu Val Val Ser Leu Ile Arg Cys Phe Phe Tyr
1 5 10 15

Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys
20 25 30

Asn Ile Trp Asp Val Ile Met Lys Met Ser Ile Ala Asp Leu Lys Lys
35 40 45

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

Lys	Glu	Val	Glu	Glu	Trp	Lys	Ser	Leu	Gly	Phe	Ala	Pro	Gly	Lys	
1				5					10				15		
Leu	Arg	Leu	Ile	Pro	Lys	Lys	Thr	Thr	Phe	Arg	Pro	Ile	Met	Thr	Phe
				20				25				30			
Asn	Lys	Lys	Ile	Val	Asn	Ser	Asp	Arg	Lys	Thr	Thr	Lys	Leu	Thr	Thr
					35		40					45			
Asn	Thr	Lys	Leu	Leu	Asn										
					50										

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

Gly	Gln	Pro	Lys	Leu	Phe	Phe	Ala	Thr	Met	Asp	Ile	Glu	Lys	Cys	Tyr
1				5					10				15		
Asp	Ser	Val	Asn	Arg	Glu	Lys	Leu	Ser	Thr	Phe	Leu	Lys	Thr	Thr	Lys
					20				25				30		
Leu	Leu														

(2) INFORMATION FOR SEQ ID NO:388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

Lys	Phe	Tyr	Lys	Gln	Thr	Lys	Gly	Ile	Pro	Gln	Gly	Leu	Cys	Val	Ser
1														15	
Ser	Ile	Leu	Ser	Ser	Phe	Tyr	Tyr	Ala	Thr	Leu	Glu	Glu	Ser	Ser	Leu
														30	
Gly	Phe	Leu													
		35													

(2) INFORMATION FOR SEQ ID NO:389:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

Leu	Met	Arg	Leu	Thr	Asp	Asp	Tyr	Leu	Leu	Ile	Thr	Thr	Gln	Glu	Asn
1														15	
Asn	Ala	Val	Leu	Phe	Ile	Glu	Lys	Leu	Ile	Asn	Val	Ser	Arg	Glu	Asn
														30	
Gly	Phe	Lys	Phe	Asn	Met	Lys	Lys	Leu	Gln	Thr					
		35								40					

(2) INFORMATION FOR SEQ ID NO:390:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

Gln	Asp	Tyr	Cys	Asp	Trp	Ile	Gly	Ile	Ser	Ile
1										10

(2) INFORMATION FOR SEQ ID NO:391:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

Trp	Leu	Phe	Arg	Gln	Leu	Ile	Pro	Lys	Ile	Ile	Gln	Thr	Phe	Phe	Tyr
1				5					10				15		
Cys	Thr	Glu	Ile	Ser	Ser	Thr	Val	Thr	Ile	Val	Tyr	Phe	Arg	His	Asp
			20					25				30			
Thr	Trp	Asn	Lys	Leu	Ile	Thr	Pro	Phe	Ile	Val	Glu	Tyr	Phe	Lys	
				35				40				45			

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

Cys	Arg	Asn	His	Asn	Ser	Tyr	Thr	Leu	Ser	Asn	Phe	Asn	His	Ser	Lys
1				5					10				15		
Met	Arg	Ile	Ile	Pro	Lys	Lys	Ser	Asn	Asn						
			20					25							

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

Phe	Arg	Ile	Ile	Ala	Ile	Pro	Cys	Arg	Gly	Ala	Asp	Glu	Glu	Phe
1				5				10				15		
Thr	Ile	Tyr	Lys	Glu	Asn	His	Lys	Asn	Ala	Ile	Gln	Pro		
			20					25						

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile Ser Thr Asp Gln Gln
1 5 10 15
Gln Val Ile Asn Ile Lys Lys Leu Ala Met Gly Gly Phe Gln Lys Tyr
20 25 30
Asn Ala Lys Ala Asn Arg Asp Lys Ile Leu Ala
35 40

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

Lys Glu Leu Glu Val Trp Lys His Ser Ser Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

Leu Ser Asn Glu Leu Gly Thr Gly Lys Phe Lys Phe Lys Pro Met Arg
1 5 10 15
Ile Val Asn Ile Pro Lys Pro Lys Gly Gly Ile Arg Pro Leu Ser Val
20 25 30
Gly Asn Pro Arg Asp Lys Ile Val Gln Glu Val Met Arg Met Ile Leu
35 40 45
Asp Thr Ile Phe Asp Lys Lys
50 55

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

Phe	Gly	Gly	Ser	Asn	Trp	Phe	Ile	Glu	Val	Asp	Leu	Lys	Lys	Cys	Phe
1						5									15
Asp	Thr	Ile	Ser	His	Asp	Leu	Ile	Ile	Lys	Glu	Leu	Lys	Arg	Tyr	Ile
						20				25				30	
Ser	Asp														

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

Thr	Tyr	His	Lys	Pro	Met	Leu	Gly	Leu	Pro	Gln	Gly	Ser	Leu	Ile	Ser
1						5									15
Pro	Ile	Leu	Cys	Asn	Ile	Val	Met	Thr	Leu	Val	Asp	Asn	Trp	Leu	Glu
						20				25				30	
Asp	Tyr	Ile													
		35													

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

Lys	Met	Ile	Lys	Arg	Asp	Leu	Asn	Asn	Phe	Leu	Asn	Ser	Leu	Gly	Leu
1									5						15

Thr Ile Asn Glu Glu Lys Thr Leu Ile
20 25

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

Arg Cys Val Val Glu Gly Thr Phe Pro Pro Val Trp Lys Asp Gly Arg
1 5 10 15
Leu Leu Val Leu Pro Lys Gly Asn Gly Arg
20 25

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

Tyr Arg Pro Val Thr Leu Leu Pro Val Leu Gly Lys Ile Leu Glu Lys
1 5 10 15
Val Leu Leu Gln Cys Ala Pro Gly Leu Thr His Ser Ile
20 25

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

Glu Gln Arg Tyr Val Met Ala Ile Phe Leu Asp Ile Ser Gly Ala Phe
1 5 10 15

Asp Asn Ala Trp Trp Pro Met Ile Met Val Lys Ala Lys Arg Asn Cys
20 25 30

Pro Pro

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

Glu Trp Lys Val Ser Thr Met Gly Cys Pro Gln Gly Ser Val Leu Gly
1 5 10 15

Pro Thr Leu Trp Asn Val Leu Met Asp Asp Leu Leu Ala Leu Pro Gln
20 25 30

Gly Ile Glu
35

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

Met Val Ala Tyr Ala Asp Asp Val Thr Val Leu Val Arg Gly Asp Ser
1 5 10 15

Arg

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

Ala His Ala Val Leu Gly Leu Ala Glu Gly Trp Ala Ser Arg Asn Lys
1 5 10 15
Leu Asp Phe Ala Pro Ala Lys Ser Arg Cys
20 25

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

Glu Asn Gln Val Thr Val Leu Gly Val Ser Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

Glu Gly Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro
1 5 10 15
Val Phe Ala Ile Lys Lys Lys Asp Ser Thr
20 25

(2) INFORMATION FOR SEQ ID NO:408:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

Trp Arg Lys Leu Val Asp Phe Arg Glu Leu Asn Lys Arg Thr Gln Asp
1 5 10 15

Phe	Trp	Glu	Val	Gln	Leu	Gly	Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys
20							25						30		
Lys	Lys	Ser	Val	Thr	Val	Leu	Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val
	35						40					45			
Pro	Leu	Asp	Glu	Asp	Phe	Arg	Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

Gly	Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser
1				5					10				15		
Pro	Ala	Ile	Phe	Gln	Ser	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Lys
			20					25				30			
Lys	Gln	Asn													
		35													

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

Ile	Tyr	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val	Gly	Ser	Asp	Leu	Glu	Ile
1				5				10					15		
Gly															

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

His Arg Thr Lys Ile Glu Glu Leu Arg Gln His Leu Leu Arg Trp Gly
1 5 10 15
Leu Thr Thr Pro Asp Lys Lys His Gln Lys Glu Pro Pro Phe Leu Trp
20 25 30
Met Gly Ile Thr Leu
35

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr
1 5 10 15
Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser
20 25 30
Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val Gln Leu
35 40 45
Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu Ala Arg Pro
50 55 60
Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu
65 70 75 80
Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr Phe Arg
85 90 95
Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys Ala Leu Phe
100 105 110
Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala
115 120 125
Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr Phe Val
130 135 140
Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr Phe Val Lys
145 150 155 160
Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr
165 170 175
Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg
180 185 190

Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala
 195 200 205
 Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg
 210 215 220
 Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val
 225 230 235 240
 Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe
 245 250 255
 Asp Val Phe Leu Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly
 260 265 270
 Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser
 275 280 285
 Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe
 290 295 300
 Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe
 305 310 315 320
 Leu Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr
 325 330 335
 Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys
 340 345 350
 Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala
 355 360 365
 Phe Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu
 370 375 380
 Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala
 385 390 395 400
 Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala
 405 410 415
 Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys
 420 425 430
 His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys
 435 440 445
 Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala
 450 455 460
 Cys Val Leu Gln Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr
 465 470 475 480
 Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile
 485 490 495
 Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly Ala Lys Gly Ala Ala
 500 505 510

Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu Cys His Gln Ala Phe
515 520 525

Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr Val Pro Leu Leu Gly
530 535 540

Ser
545

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 79 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

Ser Gln His Xaa Gln Thr Leu Leu Ala Ala Met Pro Ile Ser Arg Leu
1 5 10 15

Arg Phe Ile Pro Lys Pro Asn Trp Arg Pro Ile Val Asn Met Ser Tyr
20 25 30

Ser Met Gly Ala Arg Ala Leu Gly Arg Arg Lys Gln Ala Gln His Phe
35 40 45

Thr Gln Arg Leu Lys Thr Leu Phe Ser Met Leu Asn Tyr Glu Pro Glu
50 55 60

Pro Asp Ile Lys Leu Ile Asp Thr Ala Gln Ser Thr Ser Arg Gly
65 70 75

(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

Ser Arg Leu Arg Phe Ile Pro Lys Pro
1 5

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

Arg Pro Ile Val Asn Met
1 5

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

Leu Asn Tyr Glu
1

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

AGAGCACCGT CTGCGTGAGG AGATCCTGGC CAAGTTCTTG CACTGGCTGA TGAGTGTGTA	60
CGTCGTCGAG CTGCTCAGGT CTTTCTTTA TGTACGGAG ACCACGTTTC AAAAGAACAG	120
GCTCTTTTC TACCGGAAGA GTGTCTGGAG CAAGTTGCAA AGCATTGGAA TCAGACAGCA	180
CTTGAAGAGG GTGCAGCTGC GGGAGCTGTC GGAAGCAGAG GTCAGGCAGC ATCGGGAAAGC	240
CAGGCCCGCC CTGCTGACGT CCAGACTCCG CTTCATCCCC AAGCCTGACG GGCTGCGGCC	300
GATTGTGAAC ATGGACTACG TCGTGGGAGC CAGAACGTTC CGCAGAGAAA AGAGGGCCGA	360
GCGTCTCACCC TCGAGGGTGA AGGCACTGTT CAGCGTGCTC AACTACGAGC GGGCGCGGCCG	420

CCCCGGCCTC	CTGGGCGCCT	CTGTGCTGGG	CCTGGACGAT	ATCCACAGGG	CCTGGCGCAC	480
CTTCGTGCTG	CGTGTGCGGG	CCCAGGACCC	GCCGCCTGAG	CTGTACTTTG	TCAAG	535

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

AGAGCACCGT	CTGCGTGAGG	AGATCCTGGC	CAAGTTCCTG	CACTGGCTGA	TGAGTGTGTA	60
CGTCGTCGAG	CTGCTCAGGT	CTTTCTTTA	TGTCACGGAG	ACCACGTTTC	AAAAGAACAG	120
GCTCTTTTC	TACCGGAAGA	GTGTCTGGAG	CAAGTTGCAA	AGCATTGGAA	TCAGACAGCA	180
CTTGAAGAGG	GTGCAGCTGC	GGGAGCTGTC	GGAAGCAGAG	GTSAGKCAGC	ATCNRSARRC	240
MMKGCTAGCM	GCCMTGCYNA	YSTCSAGACT	SCGCTTCATC	CCCAAGCCYR	ACKGGCTGCG	300
GCCSATTGTG	AACATGRRYT	AYRKCRTGGG	WGCCAGARCK	TTSSGCAGAR	RRAAGMRGGC	360
CCAGCATTTC	RCCSAGCGTC	TCACCTCGAG	GGTGAAGRCW	CTSTTCAGCR	TGCTCAACTA	420
YGAGCSGGCG	CGGCRMYYCG	RYMTCMWGGG	CGCCTCTRTG	CTGGGCCTGG	ACGATATCCA	480
CAGGGCCTGG	CGCACCTTCG	TGCTGCGTGT	GCGGGCYCAG	RRCMCGYCGM	SKRGGSTGTA	540
CTTTGTCAAG						550

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

GAGTCAGCAT	CNACAGACAC	TGCTAGCAGC	CATGCCNATC	TCGAGACTGC	GCTTCATCCC	60
CAAGCCCAAC	TGGCGGCCCA	TTGTGAACAT	GAGTTATAGC	ATGGGTGCCA	GAGCTTGAGG	120
CAGAAGGAAG	CAGGCCAGC	ATTCACCCA	GCGTCTCAAG	ACTCTCTTCA	GCATGCTCAA	180
CTATGAGCCG	GAATTCGATA	TCAAGCTTAT	CGATACCGCT	CAGAGCACGT	CGAGGGGGG	239

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg	Ser	Phe	Phe	Tyr
1				5				10					15		
Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe	Phe	Tyr	Arg	Lys
	20						25						30		
Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile					
	35					40									

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

Glu	Ala	Glu	Val	Arg
1		5		

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

Ser	Arg	Leu	Arg	Phe	Ile	Pro	Lys	Pro	Asp	Gly	Leu	Arg	Pro	Ile	Val
1				5				10					15		

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr
1 5 10 15

Ile

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu
1 5 10 15

Leu Cys Ser Leu Cys Tyr
20

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

Gly	Val	Pro	Glu	Tyr	Gly	Cys	Val	Val	Asn	Leu	Arg	Lys	Thr	Val	Val
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

Trp	Cys	Gly	Leu	Leu	Leu	Asp	Thr	Arg	Thr	Leu					
1				5				10							

(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

Trp	Leu	Tyr	Asn	Ser	Phe	Ile	Ile	Pro	Ile	Leu	Gln	Ser	Phe	Phe	Tyr
1					5				10					15	

Ile	Thr	Glu	Ser	Ser	Asp	Leu	Arg	Asn	Arg	Thr	Val	Tyr	Phe	Arg	Lys
					20				25				30		

Asp	Ile	Trp	Lys	Leu	Leu	Cys	Arg	Pro	Phe	Ile					
					35			40							

(2) INFORMATION FOR SEQ ID NO:429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

Glu Asn Asn Val Arg
1 5

(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

Ala Val Ile Arg Leu Leu Pro Lys Lys Asn Thr Phe Arg Leu Ile Thr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

Arg Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys Ser Cys Tyr Asp Arg
1 5 10 15

Ile

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

Tyr	Leu	Gln	Lys	Val	Gly	Ile	Pro	Gln	Gly	Ser	Ile	Leu	Ser	Ser	Phe
1				5						10					15
Leu	Cys	His	Phe	Tyr	Met										
			20												

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

Val	Leu	Leu	Arg	Val	Val	Asp	Asp	Phe	Leu	Phe	Ile	Thr			
1				5						10					

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

Gly	Phe	Glu	Lys	His	Asn	Phe	Ser	Thr	Ser	Leu	Glu	Lys	Thr	Val	Ile
1					5					10					15

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

Phe	Phe	Gly	Phe	Ser	Val	Asn	Met	Arg	Ser	Leu					
1				5						10					

(2) INFORMATION FOR SEQ ID NO:436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

Trp	Ile	Phe	Glu	Asp	Leu	Val	Val	Ser	Leu	Ile	Arg	Cys	Phe	Phe	Tyr
1					5				10						15
Val	Thr	Glu	Gln	Gln	Lys	Ser	Tyr	Ser	Lys	Thr	Tyr	Tyr	Tyr	Arg	Lys
					20				25					30	
Asn	Ile	Trp	Asp	Val	Ile	Met	Lys	Met	Ser	Ile					
					35			40							

(2) INFORMATION FOR SEQ ID NO:437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

Glu	Lys	Glu	Val	Glu
1			5	

(2) INFORMATION FOR SEQ ID NO:438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

Gly	Lys	Leu	Arg	Leu	Ile	Pro	Lys	Lys	Thr	Thr	Phe	Arg	Pro	Ile	Met
1					5				10						15

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp Ser
1 5 10 15

Val

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys Val Ser Ser Ile
1 5 10 15

Leu Ser Ser Phe Tyr Tyr
20

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

Val Ser Arg Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu Gln Thr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

Trp Ile Gly Ile Ser Ile Asp Met Lys Thr Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

Trp Leu Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr
1 5 10 15

Cys Thr Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp
20 25 30

Thr Trp Asn Lys Leu Ile Thr Pro Phe Ile
35 40

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

Glu Asn Asn Val Cys
1 5

(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:447:

(i) SEQUENCE CHARACTERISTICS:-
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

Phe Arg Ile Ile Ala
1 5

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

Pro Glu Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr Asp Ser
1 5 10 15

Ile

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

Tyr Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro
1 5 10 15

Ile Val Asp Leu Val Tyr
20

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

Leu Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

Gly Phe Gln Lys Tyr Asn Ala Lys Ala Asn Arg Asp Lys Ile Leu Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

Trp Lys His Ser Ser Thr Met Asn Asn Phe His
1 5 10

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

Ile Pro Lys Lys
1

(2) INFORMATION FOR SEQ ID NO:454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

Leu Leu Leu Arg Leu
1 5

(2) INFORMATION FOR SEQ ID NO:455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

Asp Asp Phe Leu
1

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

GGYTTNGGDA TRAANC

16

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

GCNTAYGAYA CNAT

14

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

TANGTRTCRT ANGC

14

(2) INFORMATION FOR SEQ ID NO:459:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

GGNATHCCNC ARGG

14

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

SWNCCYTGNG GDATNCC

17

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

YTNGTNGAYG AYTTYYT

17

(2) INFORMATION FOR SEQ ID NO:462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

GTNACNARNA RRAARTCRTC

20

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

Asp Asp Phe Leu Leu Val Thr
1 5

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met, or Cys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met, or Asp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met, or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met, or Tyr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 13
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 1
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met, or Gln, Arg or Gly"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

Xaa Xaa Xaa Xaa Xaa Xaa Gln Gly Xaa Xaa Xaa Ser Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 1
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met, or His or Tyr"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 5

(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met, or Thr"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 8

(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met, or Tyr"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 9

(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met, or Tyr or Lys"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 10

(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

Xaa Xaa Xaa Xaa Xaa Asp Asp Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 2

(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met, or Cys"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 4
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met, or Lys or Thr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

Gly Xaa Xaa Xaa Xaa Xaa Xaa Lys
1 5

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 1
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met, or Cys, Lys or Tyr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 3
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met, or Ser or Tyr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 6
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met, or Tyr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 8
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met, or Arg or Gln"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met, or Cys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Thr, Lys, Tyr or Glu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met, or Asp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met, or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Glu, Lys or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Cys or Ala"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 10
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met, or Tyr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 11
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Asp or Phe"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 12
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Ser or Thr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 13
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 3
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Thr or Lys"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 4
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Met, Phe or Val"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 6
 - (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Ile or Val"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 7
 - (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Glu or Lys"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 9
 - (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Cys or Ala"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 12
 - (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Ser or Thr"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 13
 - (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Ile or Val"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

Phe Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Tyr Asp Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:471:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 2
 - (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 7
 - (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 8
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 10
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 11
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 12
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Gln or Arg"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 29
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 30
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 38
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 41
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 48
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Lys or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

Trp Xaa Phe Phe Tyr
1 5 10 15
Xaa Thr Glu Xaa Arg Xaa
20 25 30
Xaa Xaa Trp Xaa Xaa Xaa Xaa Xaa Xaa Ile Xaa Xaa Xaa Xaa Xaa
35 40 45

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 1
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 6
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 8
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Ile Pro Lys Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

Xaa Arg Xaa Xaa Pro Lys
1 5

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

Xaa Arg Xaa Ile Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 6
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 8
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 10
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

Pro Xaa Leu Tyr Phe Xaa Xaa Xaa Asp Xaa Xaa Xaa Cys Tyr Asp Xaa
1 5 10 15

Ile

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 10
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

Leu Leu Arg Leu Xaa Asp Asp Xaa Leu Xaa Ile Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

Arg Lys Xaa Xaa Trp Xaa Xaa Leu
1 5

(2) INFORMATION FOR SEQ ID NO:478:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 1
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 3
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

Xaa Arg Xaa Xaa Pro Lys
1 5

(2) INFORMATION FOR SEQ ID NO:479:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

Leu Leu Leu Arg Leu Xaa Asp Asp Phe Leu
1 5 10